

OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 08:57:52 ; Search time 4611.42 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgcac.....cctaagcataggctttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:*
- 2: gb_hrg:*
- 3: gb_in:*
- 4: gb_on:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*

- 28: em_un:*
- 29: em_vi:*
- 30: em_hrg_hum:*
- 31: em_hrg_inv:*
- 32: em_hrg_other:*
- 33: em_hrg_mus:*
- 34: em_hrg_pln:*
- 35: em_hrg_rod:*
- 36: em_hrg_mam:*
- 37: em_hrg_vrt:*
- 38: em_sy:*
- 39: em_hrgo_hum:*
- 40: em_hrgo_mus:*
- 41: em_hrgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being print ,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1803	100.0	1803	10	AF173380	AF173380 Mus muscu
2	1498.4	83.1	5219	10	BC042206	BC042206 Mus muscu
3	1487.4	82.5	5218	10	BC041777	BC041777 Mus muscu
4	1460.8	81.0	3629	10	BC043321	BC043321 Mus muscu
5	1316.6	73.0	1323	10	AY246699	AY246699 Mus muscu
6	1187	65.8	1323	10	AY208915	AY208915 Rattus no
7	1064.8	59.1	1977	9	AF293357	AF293357 Homo sapi
8	1051	58.3	3742	6	AX210037	AX210037 Sequence
9	1016	56.4	3455	9	AF121259	AF121259 Homo sapi
10	1003.6	55.7	1615	6	AX301208	AX301208 Sequence
11	928.4	51.5	5214	9	HSN800661	ALC06842 Homo sapi
12	928.4	51.5	5799	6	AX210061	AX210061 Sequence
13	928.4	51.5	5857	9	AH033114	AB033114 Homo sapi
14	924.4	51.3	3315	6	BD160624	BD160624 Primer fo
15	924.4	51.3	3315	9	AK024357	AK024357 Homo sapi
16	865.4	48.0	1758	6	AX209989	AX209989 Sequence
17	865.4	48.0	3654	6	AX209987	AX209987 Sequence
18	865.4	48.0	3813	6	AX210064	AX210064 Sequence
19	863.8	47.9	1458	6	AX209991	AX209991 Sequence
20	861.8	47.8	1191	6	AX209993	AX209993 Sequence
21	651.2	36.1	1142	9	BC017740	BC017740 Homo sapi
22	630	34.9	2895	9	BC033842	BC033842 Homo sapi
23	610	33.8	1229	10	BC030860	BC030860 Mus muscu
24	540.8	30.0	775	6	AX210002	AX210002 Sequence
25	515.8	28.6	830	6	BD149938	BD149938 Primer fo
c 26	483.2	26.8	194355	2	AC116511	AC116511 Mus muscu
27	436	24.2	270745	2	AC097544	AC097544 Rattus no
28	385.4	21.4	2548	9	AK000172	AK000172 Homo sapi
29	294.4	16.3	194355	2	AC116511	AC116511 Mus muscu
30	291.8	16.2	729	9	HUM2D67D11	AF086371 Homo sapi
31	276.6	15.3	2235	9	AK093875	AK093875 Homo sapi
c 32	241.4	13.4	174025	9	AC124069	AC124069 Homo sapi
33	239.8	13.3	2850	6	AX210056	AX210056 Sequence

34 239.8 13.3 171075 2 AC026842 Homo sapi
35 239.8 13.3 195290 9 AP006249 Homo sapi
36 237.8 13.2 4021 9 AB018317 Homo sapi
37 236.6 13.1 100000 9 AB020864 Homo sapi
38 236.6 13.1 131299 9 AF165145 Homo sapi
39 233.8 13.0 2333 6 AX210036 Sequence
40 226.8 12.6 1479 9 BC032481 Homo sapi
41 213.2 11.8 4442 10 AB093263 Mus muscu
42 205.2 11.4 1003 5 AF176665 Xenopus l
43 195 10.8 595 11 BV035724 Mus muscu
44 162 9.0 700 6 AX210048 Homo sapi
45 160.4 8.9 186901 2 AF267167 Homo sapi

ALIGNMENTS

RESULT 1
AF173380 1803 bp mRNA linear ROD 16-AUG-1999
LOCUS Mus musculus angiotensin II AT2 receptor-interacting protein mRNA,
DEFINITION complete cds.
ACCESSION AF173380
VERSION AF173380.1 GI:5733813
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1803)
REFERENCE Elbaz,N., Strosberg,A.D. and Nahmias,C.
AUTHORS Molecular characterization of ATIP, a novel angiotensin II type 2
TITLE receptor-interacting protein
JOURNAL Unpublished
2 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire,
CNRS UPR415, 22, rue Mechain, Paris 75014, France
FEATURES
source
1..1803
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/cell_line="E18"
/dev_stage="fetus"
178..1500
/note="ATIP"
/codon_start=1
/product="angiotensin II AT2 receptor-interacting protein"
/protein_id="AAD49746.1"
/db_xref="GI:5733814"

CDS
RKNPSLICQTOTAPDVLSSERTLELAQYKTCESQSGFIIHLRLISRGNNKFEAL
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KINQHQDTELEENRLKDYTAECCKLSYIEAEKTKYQLOQEPDINAAHETIK
LEIASHSEKVELLKTYETSLSEIKKSHMEKKSLDILNEKQESLEKXQINDLKEN

DAIMERKSEEQKLSREKANKPNQWYLELESLSKAVLEIKNEKLHOODIKMM
EKVDNNTALVDKLRFOENBELKAMDKMAISRQLSTEQAAQESLEAEKMKR
LSMENELLKWLNGDLCSPKSPSSAIFQSPRNSGSFSSPSISPR"
BASE COUNT 539 a 464 c 440 g 360 t
ORIGIN
Query Match 100.0%; Score 1803; DB 10; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTACCCCCCCCCACGACACCCCCCAATCTGGTGGCTGGCATTTAGCATGTAAAGCTTGT 60
Db 1 GCTACCCCCCCCCACGACACCCCCCAATCTGGTGGCTGGCATTTAGCATGTAAAGCTTGT 60
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Db 121 TGATGGTCCCTGGAAAAGCTGCTTCCCTGGGAAAGTTCTCCACATGGCTTCGAAAGCATG 180
QY 181 CTGTTGTCCTCCCAATCTCCTATCCACATCCAGCTCCGCTAACGCGCAAGGACTG 240
Db 181 CTGTTGTCCTCCCAATCTCCTATCCACATCCAGCTCCGCTAACGCGCAAGGACTG 240
QY 241 CTTCGAAACTCCGGCTTCTTCGGGGCTCAGGAAAAACACTGTCAATTTCCACACACTT 300
Db 241 CTTCGAAACTCCGGCTTCTTCGGGGCTCAGGAAAAACACTGTCAATTTCCACACACTT 300
QY 301 GAAAGGGGAGGAGAGAAATCCACAGAGCTGTGCATCCACACACAGAGCTCCAGAT 360
Db 301 GAAAGGGGAGGAGAGAAATCCACAGAGCTGTGCATCCACACACAGAGCTCCAGAT 360
QY 361 GTGCTGTCTCCGAGAGAGAGCTTGAGTTGGCCCAATACAGACAAAATGTGAAGCCAA 420
Db 361 GTGCTGTCTCCGAGAGAGAGCTTGAGTTGGCCCAATACAGACAAAATGTGAAGCCAA 420
QY 421 AGTGGATTCACTCTGCACCTCAGGACGCTTCTTCCTGGTGTAAACAACAAGTTTGAAGCT 480
Db 421 AGTGGATTCACTCTGCACCTCAGGACGCTTCTTCCTGGTGTAAACAACAAGTTTGAAGCT 480
QY 481 CTGACAGTTGTGATCCAGACCTCTGTGTGAGCGGGAGGAGGAGCTGAGGCAACAA 540
Db 481 CTGACAGTTGTGATCCAGACCTCTGTGTGAGCGGGAGGAGGAGCTGAGGCAACAA 540
QY 541 ACCCTCTCTCAAGAACTTGTGAGCTCCGGGAGAGAGCTAGTTGCTGTCAAGCGCTGT 600
Db 541 ACCCTCTCTCAAGAACTTGTGAGCTCCGGGAGAGAGCTAGTTGCTGTCAAGCGCTGT 600
QY 601 GAGAGCTAGAAAAGGCTAGGCTGACTTACACAGACAGGCTATCAAGAATTTGTCCAGAA 660
Db 601 GAGAGCTAGAAAAGGCTAGGCTGACTTACACAGACAGGCTATCAAGAATTTGTCCAGAA 660
QY 661 CTAAACGACGACATCAGACAGACCGGACGACTGGAGACCGGCTGAGGACTTATAC 720
Db 661 CTAAACGACGACATCAGACAGACCGGACGACTGGAGACCGGCTGAGGACTTATAC 720

QY 1561 CTCTCATGGGAAGTCTGAGTTGCTGGCTTAGCTCTCTGGAATATCCACAGGATATCGGGAG 1620
|||||
Db 1561 CTCTCATGGGAAGTCTGAGTTGCTGGCTTAGCTCTCTGGAATATCCACAGGATATCGGGAG 1620
QY 1621 AGCAGCGCGCAACCGTATCAGCTAGCTAGCAATAGAGAGCTCCAATAGAGACTTTTAAAC 1680
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Db 1621 AGCAGCGCGCAACCGTATCAGCTAGCTAGCAATAGAGAGCTCCAATAGAGACTTTTAAAC 1680
QY 1681 TTGGTCCAAAAGGCTCTCTCCAAAAACAGATTTCGGAACTGAAAGTGGACATAGTTGCACAA 1740
|||||
Db 1681 TTGGTCCAAAAGGCTCTCTCCAAAAACAGATTTCGGAACTGAAAGTGGACATAGTTGCACAA 1740
QY 1741 AGCACTTACGGAAAGGAGGAACTTTGTTCTTTGGCTTCTTCACTTAAGCATAGGCTTTC 1800
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Db 1741 AGCACTTACGGAAAGGAGGAACTTTGTTCTTTGGCTTCTTCACTTAAGCATAGGCTTTC 1800
QY 1801 CAG 1803
|||
Db 1801 CAG 1803
Search completed: October 21, 2003, 17:17:49
Job time : 4620.42 secs

QY 721 ACCGACAGGTGTGAGAGCTTCAGAGCATTTACATTTGAGGAGCGCAAAATATATAAACT 780
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Db 721 ACCGACAGGTGTGAGAGCTTCAGAGCATTTACATTTGAGGAGCGCAAAATATATAAACT 780
QY 781 CAATCTCAAGAGCAGTTTGACCACTTTAAAGCGCGCCCAATAGAGACCACTTAAGCTTGAGATT 840
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Db 781 CAATCTCAAGAGCAGTTTGACCACTTTAAAGCGCGCCCAATAGAGACCACTTAAGCTTGAGATT 840
QY 841 GAGCTTAGCCACTCGGAGAAAGTGGATTCCTGAAAGACCTTAGAAACCTCCCTTTCA 900
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Db 841 GAGCTTAGCCACTCGGAGAAAGTGGATTCCTGAAAGACCTTAGAAACCTCCCTTTCA 900
QY 901 GAAATCAAGAGAGCCATGAGATGGAGAGAGTCACTGGAGATCTGCTTAATGAGAG 960
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Db 901 GAAATCAAGAGAGCCATGAGATGGAGAGAGTCACTGGAGATCTGCTTAATGAGAG 960
QY 961 CAGGAATCGCTGGAGAAACAAATCAATGATCTGAAGAGTGAAGAGCTGCTTTAAACGAA 1020
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Db 961 CAGGAATCGCTGGAGAAACAAATCAATGATCTGAAGAGTGAAGAGCTGCTTTAAACGAA 1020
QY 1021 AGGTTGAATCAGAGGAGCAAAAGCACTGTCAAGAGAGAGCGCAATTCCAAAAACCT 1080
|||||
Db 1021 AGGTTGAATCAGAGGAGCAAAAGCACTGTCAAGAGAGAGCGCAATTCCAAAAACCT 1080
QY 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCTGAAGGCTGTGTAGAGATCAAGAT 1140
|||||
Db 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCTGAAGGCTGTGTAGAGATCAAGAT 1140
QY 1141 GAGAGCTGCACCGAGAGCATGAAGCTAATGAGATGAAAGCTGGAGACATTAAC 1200
|||||
Db 1141 GAGAGCTGCACCGAGAGCATGAAGCTAATGAGATGAAAGCTGGAGACATTAAC 1200
QY 1201 ACAGCATTGTTGACAAAGCTGAAGGATTCAGAGGAAACAGAGGTTAAAGCTCGC 1260
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Db 1201 ACAGCATTGTTGACAAAGCTGAAGGATTCAGAGGAAACAGAGGTTAAAGCTCGC 1260
QY 1261 ATGGACAAACATGGCAATTTCAAGGCAACTTTCACCGAGAGCGCGCGCTGCAAGAG 1320
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Db 1261 ATGGACAAACATGGCAATTTCAAGGCAACTTTCACCGAGAGCGCGCGCTGCAAGAG 1320
QY 1321 TCCCTTGAGAGAGGTCAAAGGTCAAAGAGACTGTCCATGGAGAAAGAGGAACTTCG 1380
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Db 1321 TCCCTTGAGAGAGGTCAAAGGTCAAAGAGACTGTCCATGGAGAAAGAGGAACTTCG 1380
QY 1381 TGGAACTGCAACAGGAGACTGTGAGGCGCCCAAGATCCCCCAGCTCTCGGCGATC 1440
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Db 1381 TGGAACTGCAACAGGAGACTGTGAGGCGCCCAAGATCCCCCAGCTCTCGGCGATC 1440
QY 1441 CTTTTCAGTCCCCCAAGAAATTCGTTCTCTCAGGCCAGCATCTCACCCAGATGA 1500
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Db 1441 CTTTTCAGTCCCCCAAGAAATTCGTTCTCTCAGGCCAGCATCTCACCCAGATGA 1500
QY 1501 CGGCTTCTGAGCGAGGAGACTCTGTGAGGAGACTGAGGTCGCTTCTGAGGACTGACC 1560
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Db 1501 CGGCTTCTGAGCGAGGAGACTCTGTGAGGAGACTGAGGTCGCTTCTGAGGACTGACC 1560

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 ; Search time 346.674 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgac.....cctaagcatagctttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1803	100.0	1803	21	AAZ99088
2	1323	73.4	1323	21	AAZ99089
3	1051	58.3	3742	21	AAZ99091
4	1051	58.3	3742	22	AAH74362
5	1003.6	55.7	1615	24	AAZ99905
6	941.8	52.2	1308	21	AAZ99092
7	925.2	51.3	5799	22	AAH74383
8	924.4	51.3	3315	22	AAH18632
9	924.2	51.3	4937	25	ABX63076
10	923.6	51.2	5961	22	AAH74385
11	886.6	49.2	1369	22	AAH74322
12	868.4	48.2	3807	25	ABX10230
13	865.4	48.0	1758	22	AAH74324
14	865.4	48.0	3654	22	AAH74323
15	863.8	47.9	1458	22	AAH74325
16	861.8	47.8	1191	22	AAH74326
17	844.8	35.8	910	24	ABSS1467
18	540.8	30.0	775	22	AAH74327
19	521.4	28.9	3287	21	AAF22392
20	515.8	28.6	830	22	AAH07946
21	354	19.6	354	21	AAZ99090
22	342.2	19.0	656	22	AAZ6578
23	342.2	19.0	656	25	ABX73919
24	337	18.7	791	25	AAZ53121
25	304.6	16.9	481	22	AAZ62163
26	304.6	16.9	481	25	ABX73504
27	239.8	13.3	2850	22	AAH74380
28	237.8	13.2	4184	25	ABX71114
29	233.8	13.0	2333	22	AAH74361
30	212.8	11.8	435	25	ABX53761
31	174.8	9.7	242	25	ABX74609
32	162	9.0	700	22	AAH74372
33	159	8.8	215	22	AAH74353
34	143	7.9	900	22	AAH74371
35	143	7.9	2672	24	ABK09997
36	142.6	7.9	413	22	AAH74352
37	138.6	7.7	367	22	AAH74329
38	130	7.2	338	21	AAA41587
39	128	7.1	562	23	ABV48083
40	106.6	5.9	700	22	AAH74374
41	104.2	5.8	133	24	ABV88907
42	102.8	5.7	203	22	AAH74355
43	93.4	5.2	600	22	AAH74378
44	92.8	5.1	120	22	AAH74363
45	91.8	5.1	1370	22	AAZ06852

ALIGNMENTS

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCTACCCGCCCCCAGCACACCCCAATCTGGGTGGCTGGCATTAGCATGTAAGCTTGT	60
DB	1	GCTACCCGCCCCCAGCACACCCCAATCTGGGTGGCTGGCATTAGCATGTAAGCTTGT	60
QY	61	TTTTCTCTGGCTGTATCTCTGGGCTGGAAAGAACCCGAGTTGCCAAGACACAGTAT	120
DB	61	TTTTCTCTGGCTGTATCTCTGGGCTGGAAAGAACCCGAGTTGCCAAGACACAGTAT	120
QY	121	TGATGGTCCCTGGAAAAGCTGCTTCCCTGCGAAGTTCTCCACTGCGTTCGAAGCAT	180
DB	121	TGATGGTCCCTGGAAAAGCTGCTTCCCTGCGAAGTTCTCCACTGCGTTCGAAGCAT	180
QY	181	CTGTGTCTCCCAANTCTCTTATCCACATCCAGCTCCGCTAACCGCAAGACAT	240
DB	181	CTGTGTCTCCCAANTCTCTTATCCACATCCAGCTCCGCTAACCGCAAGACAT	240
QY	241	CTTCGAACCTCCGGCTTCCTTCGGGGCTCAGGAAAAACACTGTCTATTTCCACAGT	300
DB	241	CTTCGAACCTCCGGCTTCCTTCGGGGCTCAGGAAAAACACTGTCTATTTCCACAGT	300
QY	301	GAAGGGGAGGAGAGAGATCCAGAGGCTGTGCTATCCAGACCCAGACAGTCCAGAT	360
DB	301	GAAGGGGAGGAGAGAGATCCAGAGGCTGTGCTATCCAGACCCAGACAGTCCAGAT	360
QY	361	GTGTGTCTCCGAGAGACGCTTGAGTTGGGCCAATACAGACAAAATGTGAAGCCAA	420
DB	361	GTGTGTCTCCGAGAGACGCTTGAGTTGGGCCAATACAGACAAAATGTGAAGCCAA	420
QY	421	AGTGGATTCACTCTGACACCTCAGGAGCTTCTTCCCGTGGTAAACAACAAGTGAAGCG	480
DB	421	AGTGGATTCACTCTGACACCTCAGGAGCTTCTTCCCGTGGTAAACAACAAGTGAAGCG	480
QY	481	CTGACAGTTGTATCCAGCACTCTCTGAGCGGGAGGAGGAGCTGAGGACACAAA	540
DB	481	CTGACAGTTGTATCCAGCACTCTCTGAGCGGGAGGAGGAGCTGAGGACACAAA	540
QY	541	ACCTCTCTCAAGAACTTGTGAGGCTCCGGGAGAGCTAGTTGCTTCAAGCGCTGT	600
DB	541	ACCTCTCTCAAGAACTTGTGAGGCTCCGGGAGAGCTAGTTGCTTCAAGCGCTGT	600
QY	601	GAGAGCTAGAAAAGGCTAGGCTGACTTACAGACAGCGTATCAAGAATTTGTCCAGAAA	660
DB	601	GAGAGCTAGAAAAGGCTAGGCTGACTTACAGACAGCGTATCAAGAATTTGTCCAGAAA	660
QY	661	CTAAACGACGAGATCAGACAGACCGGAGGAGCTGAGAGACCGGCTGAGGAGCTTATAC	720
DB	661	CTAAACGACGAGATCAGACAGACCGGAGGAGCTGAGAGACCGGCTGAGGAGCTTATAC	720
QY	721	ACCGCAGAGTGTGAGAGCTTCAAGACATTTACATTGAGGAGGAGAGAAAATATATAACT	780
DB	721	ACCGCAGAGTGTGAGAGCTTCAAGACATTTACATTGAGGAGGAGAGAAAATATATAACT	780
QY	781	CACTCCAGAGAGAGTGTGACACTTAAACGCGCGCCATGAGACCATTAAGCTTGAAGTT	840
DB	781	CACTCCAGAGAGAGTGTGACACTTAAACGCGCGCCATGAGACCATTAAGCTTGAAGTT	840

RESULT 1
AAZ99086
ID AAZ99086 standard; cDNA; 1803 BP.
XX AC AAZ99086;
XX DT 21-JUN-2000 (first entry)
XX DE Mouse ATIP gene.
XX KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
XX KW two-hybrid screen; signal transduction.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 178
XX FT /*tag= a
XX FT /product= "ATIP"
XX FT /note= "angiotensin II (AT2) receptor interactive
XX FT protein"
XX PN FR2782064-A1.
XX PD 11-FEB-2000.
XX PF 04-AUG-1996; 98FR-0009997.
XX PR 04-AUG-1996; 98FR-0009997.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Elbaz N, Nahmias C, Strosberg AD;
XX WPI; 2000-248410/22.
XX P-PSDB; AAY83777.
XX PT Nucleic acids coding for angiotensin II receptor AT2 interacting
XX PT proteins useful in screening assays for receptor-protein interaction -
XX PS Claim 1; Fig 3; 63pp; French.
XX CC This sequence represents the cDNA encoding a mouse angiotensin II (AT2)
XX CC receptor interactive protein (ATIP). The gene was isolated from a
XX CC two-hybrid screen using the C-terminal fragment of the mouse AT2
XX CC receptor as the "bait" (AAY83781). The "target" is a mouse foetal cDNA
XX CC library. Cells transformed with vectors containing the cDNA, or
XX CC immobilized proteins encoded by it, can be used to screen for substances
XX CC that modulate ATIP-AT2 interaction or substances that interact with
XX CC ATIP, especially using yeast two- or three-hybrid techniques. Such
XX CC substances may be useful for treating disorders associated with anomalous
XX CC AT2 receptor signal transduction.
XX SQ Sequence 1803 BP; 539 A; 464 C; 440 G; 360 T; 0 other;
Query Match 100.0%; Score 1803; DB 21; Length 1803;

Dp 781 CAAGTGAAGAGAGTTTGAACAATTAAAGCGCGCCCATGAGACCACTAAGCTTGAGATT 840

QY 841 GAGCTAGCCACTGGAGAAGCTGGAAATGCTGAAGAAGACCTATGAACCTCCCTTCA 900

Dp 841 GAGCTAGCCACTGGAGAAGCTGGAAATGCTGAAGAAGACCTATGAACCTCCCTTCA 900

QY 901 GAAATCAAGAAGACCATGAGATGGAGAAGAGTCACTGGAGATCTGCTTAATGAGAAG 960

Dp 901 GAAATCAAGAAGACCATGAGATGGAGAAGAGTCACTGGAGATCTGCTTAATGAGAAG 960

QY 961 CAGGAATCCCTGGAGAAGCAAAATCAATGATCTGAAGATGAAAACGATGCTTAAACGAA 1020

Dp 961 CAGGAATCCCTGGAGAAGCAAAATCAATGATCTGAAGATGAAAACGATGCTTAAACGAA 1020

QY 1021 AGGTTGAATCAGAGAGCAAAACCACTGTCAAGAGAGAGCGCAATTCAAAAACCT 1080

Dp 1021 AGGTTGAATCAGAGAGCAAAACCACTGTCAAGAGAGAGCGCAATTCAAAAACCT 1080

QY 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCTGAAGCTGTGTAGAGATCAAGAA 1140

Dp 1081 CAGGTCATGTATCTGGAGCAAGACTAGAAAGCTGAAGCTGTGTAGAGATCAAGAA 1140

QY 1141 GAGAAGCTGCACGAGAGACATGAAGCTAATGAAGTGGAAAGCTGCTGGACATAC 1200

Dp 1141 GAGAAGCTGCACGAGAGACATGAAGCTAATGAAGTGGAAAGCTGCTGGACATAC 1200

QY 1201 ACAGCATTTGTTGAAGCTGAAGCAATCCAGAGGAAACGAGAGTTAAAGCTGCG 1260

Dp 1201 ACAGCATTTGTTGAAGCTGAAGCAATCCAGAGGAAACGAGAGTTAAAGCTGCG 1260

QY 1261 ATGACAAACACATGGCAATTTCAAGGCAACTTCCACGAGAGCGCGCTGCAAGAG 1320

Dp 1261 ATGACAAACACATGGCAATTTCAAGGCAACTTCCACGAGAGCGCGCTGCAAGAG 1320

QY 1321 TCCCTTGAGAGAGTCAAGAGTCAAGAGACTGTCCATGGAGAACGAGGAATCTTG 1380

Dp 1321 TCCCTTGAGAGAGTCAAGAGTCAAGAGACTGTCCATGGAGAACGAGGAATCTTG 1380

QY 1381 TGGAACTGCACAGGAGACTGTGAGGCCCCAAGAGATCCCCCACTCTCTGGCCATC 1440

Dp 1381 TGGAACTGCACAGGAGACTGTGAGGCCCCAAGAGATCCCCCACTCTCTGGCCATC 1440

QY 1441 CTTTCCATCCCGAGGAATCTGTTCTCTGAGGCACTGAGTGGCTTCTGAGGACTGACC 1500

Dp 1441 CTTTCCATCCCGAGGAATCTGTTCTCTGAGGCACTGAGTGGCTTCTGAGGACTGACC 1500

QY 1501 CGGCTTCTGAAGCAGAGACTCTCTGAAGCACTGAGTGGCTTCTGAGGACTGACC 1560

Dp 1501 CGGCTTCTGAAGCAGAGACTCTCTGAAGCACTGAGTGGCTTCTGAGGACTGACC 1560

QY 1561 CTCTCATGGGAATCGAGTTGCTGGTTAGCTCTCTGGAATATCCCCAGGAATCGGGAG 1620

Dp 1561 CTCTCATGGGAATCGAGTTGCTGGTTAGCTCTCTGGAATATCCCCAGGAATCGGGAG 1620

QY 1621 AGGAGCGGCAACCTATCAGCTAGTACGAATAGAGAGCTCCCAATAGAGACTTTTAC 1680

Dp 1621 AGGAGCGGCAACCTATCAGCTAGTACGAATAGAGAGCTCCCAATAGAGACTTTTAC 1680

QY 1681 TTGGTCCAAAAGCTCTCCAAAAACAGATTTGGAACTGAAGTGGACATAGTTGCACAA 1740

Dp 1681 TTGGTCCAAAAGCTCTCCAAAACAGATTTGGAACTGAAGTGGACATAGTTGCACAA 1740

QY 1741 AGCACTTAGGAGACGAGGGAACCTTGTCTTTGGCTTCCCTCACCTAAGCTAGGCTTTC 1800

Dp 1741 AGCACTTAGGAGACGAGGGAACCTTGTCTTTGGCTTCCCTCACCTAAGCTAGGCTTTC 1800

QY 1801 CAG 1803

Dp 1801 CAG 1803

Search completed: October 21, 2003, 11:10:58
Job time : 353.674 secs

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 368.905 Seconds
(without alignments)
13107.136 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgcac.....cctaagcataggtttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:**
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6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:**
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:**
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:**
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:**
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:**
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:**
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:**
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:**
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:**
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:**

1	924.2	51.3	4937	13	US-10-044-090-76	Sequence 71, Appl
2	644.8	35.8	910	14	US-10-043-487-47	Sequence 47, Appl
3	342.2	19.0	656	10	US-09-764-864-757	Sequence 757, App
4	304.6	16.9	481	10	US-09-764-864-342	Sequence 343, App
5	271.4	15.1	490	11	US-09-918-995-5132	Sequence 513, Ap
6	212.8	11.8	435	10	US-09-983-965-3690	Sequence 363, Ap
7	166.2	9.2	464	11	US-09-918-995-5569	Sequence 5569, Ap
8	159.4	8.8	444	11	US-09-918-995-12481	Sequence 12481, A
9	156.8	8.7	1117	13	US-10-027-632-85144	Sequence 85144, A
10	131.8	7.3	440	11	US-09-918-995-11578	Sequence 11578, A
11	104.2	5.8	133	10	US-09-998-598-2218	Sequence 2218, Ap
12	91.4	5.1	567	9	US-09-925-302-132	Sequence 132, App
13	67	3.7	3489	12	US-10-294-804-1	Sequence 1, Appl
14	55.2	3.1	628	12	US-10-029-386-22859	Sequence 22859, A
15	54.4	3.0	536	12	US-10-029-386-19974	Sequence 19974, A
16	54.4	3.0	599	12	US-10-029-386-6243	Sequence 6243, Ap
17	54.2	3.0	32069	12	US-10-004-113-7	Sequence 7, Appl
18	51.8	2.9	720	13	US-10-101-487-74	Sequence 74, Appl
19	51.8	2.9	720	13	US-10-101-487-76	Sequence 76, Appl
20	50.2	2.8	575	9	US-09-864-761-20733	Sequence 20733, A
21	50.2	2.8	1969	9	US-09-864-761-3972	Sequence 3972, Ap
22	49.8	2.8	8895	9	US-09-764-853-887	Sequence 887, App
23	49.8	2.8	8895	9	US-09-764-853-937	Sequence 937, App
24	49.8	2.8	8895	14	US-10-091-438-250	Sequence 250, App
25	49.8	2.8	8895	14	US-10-091-438-256	Sequence 886, App
26	49.8	2.8	9656	9	US-09-764-853-886	Sequence 933, App
27	49.8	2.8	9656	9	US-09-764-853-933	Sequence 246, App
28	49.8	2.8	9656	14	US-10-091-438-246	Sequence 255, App
29	49.8	2.8	9656	14	US-10-091-438-255	Sequence 18355, A
30	49.6	2.8	423	9	US-09-864-761-18355	Sequence 6203, Ap
31	49.4	2.7	475	9	US-09-864-761-6203	Sequence 22817, A
32	49.4	2.7	511	9	US-09-864-761-22817	Sequence 157, App
33	48.2	2.7	2313	10	US-09-738-973-157	Sequence 157, App
34	48.2	2.7	2313	10	US-09-854-133-157	Sequence 157, App
35	48.2	2.7	2313	14	US-10-144-649A-157	Sequence 157, App
36	48.2	2.7	2314	10	US-09-764-869-12	Sequence 12, Appl
37	48.2	2.7	2802	12	US-10-233-045-35	Sequence 35, Appl
38	47	2.6	3809	13	US-10-001-870-68	Sequence 60, Appl
39	46.6	2.6	541	12	US-10-029-386-12333	Sequence 12333, A
40	46.6	2.6	1040	12	US-10-029-386-26033	Sequence 26033, A
41	46.6	2.6	1371	10	US-09-938-842A-85	Sequence 85, Appl
42	46.2	2.6	700	9	US-09-864-761-17529	Sequence 1752, A
43	46	2.6	6668	12	US-10-311-455-1670	Sequence 1670, Ap
44	45.8	2.5	272	9	US-09-864-761-18684	Sequence 18684, A
45	45.6	2.5	659158	10	US-09-771-208-20	Sequence 20, Appl

Search completed: October 22, 2003, 03:34:38
Job time : 371.905 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
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OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 09:08:27 ; Search time 2842.6 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-1
Perfect score: 1803
Sequence: 1 gctacccccccacgcac.....cctaagcataggctttccag 1803

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_phg:*
27: em_gss_vri:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1750.2	97.1	2477	11	AK030510	AK030510 Mus muscu
2	1732.6	96.1	3963	11	AK031693	AK031693 Mus muscu
3	1249.6	69.3	3237	11	AK035576	AK035576 Mus muscu
4	896.6	49.7	950	13	BQ921402	BQ921402 AGENCOURT
5	845.8	46.9	920	13	BQ523654	BQ523654 AGEICOURT
6	618.4	34.3	712	10	BB567855	BB567855 BB56 855
7	614.2	34.1	1005	13	BQ070423	BQ070423 AGENCOURT
8	604.4	33.5	657	10	BB628131	BB628131 BB628131
9	598	33.2	623	10	BF577785	BF577785 602092084
10	595.2	33.0	748	10	BF141309	BF141309 601798830
11	593.8	32.9	907	13	BQ593171	BQ593171 AGENCOURT
12	592	32.8	624	12	BM951991	BM951991 UI-M-EHO-
13	583	32.3	937	10	BF607509	BF607509 MY_00045
14	579.6	32.1	782	13	BQ702398	BQ702398 UI-M-FIO-
15	567.4	31.5	734	14	CB316595	CB316595 AGENCOURT
16	564.6	31.3	600	13	BQ921755	BQ921755 6093-85 M
17	562.8	31.2	742	13	BQ204579	BQ204579 UI-R-D21-
18	552	30.6	553	12	BG800655	BG800655 0051-47 M
19	538.4	29.9	541	4	BX512030	BX512030 NZPD Mus
20	536	29.7	605	12	BF654474	BF654474 603281030
21	535.4	29.7	648	10	BB656106	BB656106 BB656106
22	529.8	29.4	639	12	BM946483	BM946483 UI-M-EMO-
23	523.4	29.0	782	9	AU141757	AU141757 AU141757
24	516	28.6	1346	11	BQ007328	BQ007328 Homo sapi
25	515.8	28.6	830	9	AU138373	AU138373 AU138373
26	513.8	28.5	517	10	BB652532	BB652532 UI-M-AMO-
27	510.6	28.3	530	13	BQ830956	BQ830956 LL61n1027
28	508.6	28.2	710	14	CB723104	CB723104 UI-M-GHO-
29	508.4	28.2	560	14	CD565243	CD565243 B0491H11-
30	504.2	28.0	711	14	BY739988	BY739988 BY739988
31	502.8	27.9	509	12	BF1319660	BF1319660 iel4a05.y
32	498.4	27.6	500	9	AA880300	AA880300 vx39f05.r
33	494	27.4	629	10	BB662397	BB662397 BB662397
34	491.4	27.3	600	13	BQ925066	BQ925066 7111-61 M
35	485.4	26.9	487	10	BF535672	BF535672 602054069
36	485	26.9	634	14	BY740600	BY740600 BY740600
37	480	26.6	778	10	BB895149	BB895149 601436077
38	478.8	26.6	728	13	BQ745000	BQ745000 UI-M-EHO-
39	477.8	26.5	630	10	BB617931	BB617931 BB617931
40	477.8	26.5	664	14	BY726879	BY726879 BY726879
41	467.4	25.9	469	14	CA531568	CA531568 C03-1B05-
42	466.8	25.9	792	12	BQ042290	BQ042290 UI-M-EHO-
43	463.4	25.7	474	9	AA980079	AA980079 ua28c.1.r
44	459.8	25.3	732	12	BM951385	BM951385 UI-M-EHO-
45	451.6	25.0	626	12	BM737916	BM737916 R-ES-0001

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 3383.75 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-3

Perfect score: 1323

Sequence: 1 atgtgtgtgtctcccaatt.....ccagcatctcaccagatga 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_nu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rdt:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1323	100.0	1803	10	AF173380	AF173380 Mus muscu
2	1316.6	99.5	1323	10	AY246699	AY246699 Mus muscu
3	1203.4	91.0	5218	10	BC041777	BC041777 Mus muscu
4	1203.4	91.0	5219	10	BC042206	BC042206 Mus muscu
5	1193.8	90.2	3629	10	BC043321	BC043321 Mus muscu
6	1187	89.7	1323	10	AY208915	AY208915 Rattus no
7	956.2	72.3	1977	9	AF293357	AF293357 Homo sapi
8	956.2	72.3	3455	9	AF121259	AF121259 Homo sapi
9	953	72.0	1615	6	AX301208	AX301208 Sequence
10	941.8	71.2	3742	6	AX210037	AX210037 Sequence
11	865.4	65.4	1758	6	AX209989	AX209989 Sequence
12	865.4	65.4	3654	6	AX209987	AX209987 Sequence
13	865.4	65.4	3813	6	AX210064	AX210064 Sequence
14	865.4	65.4	5799	6	AX210061	AX210061 Sequence
15	865.4	65.4	5857	9	AB033114	AB033114 Homo sapi
16	864.6	65.4	3315	6	BD160624	BD160624 Primer fo
17	864.6	65.4	3315	9	AK024357	AK024357 Homo sapi
18	863.8	65.3	1458	6	AX209591	AX209591 Sequence
19	863.8	65.3	5214	9	HS0800681	AL056642 Homo sapi
20	861.8	65.1	1191	6	AX209993	AX209993 Sequence
21	602.4	45.5	1142	9	BC017740	BC017740 Homo sapi
22	570.2	43.1	2895	9	BC033842	BC033842 Homo sapi
23	518	39.2	775	6	AX210002	AX210002 Sequence
24	515.8	39.0	830	6	BD149538	BD149538 Primer fo
25	325.6	24.6	2548	9	AK000172	AK000172 Homo sapi
26	315	23.6	1229	10	BC030860	BC030860 Mus muscu
27	250.6	18.9	729	9	H0MZD67D11	AF066371 Homo sapi
28	250.6	18.9	2235	9	AK093875	AK093875 Homo sapi
29	235.4	17.8	4021	9	AB018317	AB018317 Homo sapi
30	224.4	17.0	1479	9	BC032481	BC032481 Homo sapi
31	216.2	16.3	194355	2	AC116511	AC116511 Mus muscu
32	212.2	16.0	4445	10	AB093263	AB093263 Mus muscu
33	205.2	15.5	1003	5	AF176665	AF176665 Xenopus l

ALIGNMENTS

RESULT 1
AF173380
LOCUS Mus musculus angiotensin II AT2 receptor-interacting protein mRNA, complete cds.
DEFINITION AF173380 1803 bp mRNA linear ROD 16-AUG-1999
ACCESSION AF173380
VERSION AF173380.1 GI:5733813
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ORGANISM 1 (bases 1 to 1803)
REFERENCE 1 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Molecular characterization of ATIP, a novel angiotensin II type 2 receptor-interacting protein
JOURNAL Unpublished
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire, CNRS UPR415, 22, rue Mechain, Paris 75014, France
FEATURES
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TVV7OHLISEREELAKOHTLSQELVSLRGELVAASSACEKLEKARADQLTVQEFVQ
KLNQOQDTRELENRLKDYTABCEKLSIYIEABKYKTKQSQGFNLNAAHETTK
LEIFASHSEKVELLKRTYTSUSEIKKSHENKKSLEDLNKKQESLEKQDLNRSEN

BASE COUNT 539 a 464 c 440 g 360 t
ORIGIN
DALNRLKSEOKQLSREKNSKNPQVMYLEQELSLKAVLEIKNEKLHOODMKMM
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LSNEBELLMKLIENGDLCSKPSRPTSSAIFQSPRNSGSFSPSPISPR"

Query Match 100.0%; Score 1323; DB 10; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGTCTCCCAAAATTCCTTATCCACCATCCACGTCGCTTAACGCGCAAGA 60
DB 178 ATGCTGTTGTCTCCCAAAATTCCTTATCCACCATCCACGTCGCTTAACGCGCAAGA 237
QY 61 CTGCTTCGAAACCTCCGGCTTCCTTCCGCGCTCAGGAAACACACTGTCAATTTCCACACA 120
DB 238 CTGCTTCGAAACCTCCGGCTTCCTTCCGCGCTCAGGAAACACACTGTCAATTTCCACACA 297
QY 121 GTTGAAGGGGCAAGGCAAGAAATCCACAGAGGCTGTGCATCCAGACCCAGACAGCTCCA 180
DB 298 GTTGAAGGGGCAAGGCAAGAAATCCACAGAGGCTGTGCATCCAGACCCAGACAGCTCCA 357
QY 181 GATGTCGTCTCTCCGAGAGACGCTTGAGTTGGCCCAATACAGACAAATGTGAAGC 240
DB 358 GATGTCGTCTCTCCGAGAGACGCTTGAGTTGGCCCAATACAGACAAATGTGAAGC 417
QY 241 CAAAGTGGATTCACTCGACCTCAGGCGAGCTTCCTTCCTGGTAAACAAGTTTGA 300
DB 418 CAAAGTGGATTCACTCGACCTCAGGCGAGCTTCCTTCCTGGTAAACAAGTTTGA 477
QY 301 GCGCTGACAGTTGTGATCCAGCACTCTCTGTCTGAGGCGGAGAGAGCTGAGAGCAAC 360
DB 478 GCGCTGACAGTTGTGATCCAGCACTCTCTGTCTGAGGCGGAGAGAGCTGAGAGCAAC 537
QY 361 AARACCTCTCTCAGAACTTGTCAAGCTCCGCGGAGAGCTAGTTGCTGCTTCAAGCGC 420
DB 538 AARACCTCTCTCAGAACTTGTCAAGCTCCGCGGAGAGCTAGTTGCTGCTTCAAGCGC 597
QY 421 TGTGAGAACTAGAAAAGGCTAGGCTGACTTACAGACAGCGTATCAAGAAATTTGTCAG 480
DB 598 TGTGAGAACTAGAAAAGGCTAGGCTGACTTACAGACAGCGTATCAAGAAATTTGTCAG 657
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RESULT 2

AY246699
LOCUS AY246699 1323 bp mRNA linear ROD 10-APR-2003
DEFINITION Mus musculus MTSG1 mRNA, complete cds.
ACCESSION AY246699
VERSION AY246699.1 GI:29725653
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1323)
 AUTHORS Seibold,S., Wanner,C. and Galle,J.
 TITLE Cloning and characterization of MTS1
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1323)
 AUTHORS Seibold,S., Wanner,C. and Galle,J.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2003) Department of Medicine, University of
 Wuerzburg, Josef Schneider Str 2, Wuerzburg 97080, Germany
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GenCore version 5.1.6
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Run on: October 21, 2003, 08:56:18 : Search time 254.382 Seconds
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Searched: 2552736 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	941.8	71.2	3742	22	AAH74362
7	865.4	65.4	1758	22	AAH74324
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15	862.2	65.2	5961	22	AAH74385
16	861.8	65.1	1191	22	AAH74326
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19	515.8	39.0	830	22	AAH07946
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24	337	25.5	791	25	AD53121
25	304.6	23.0	481	22	AS26163
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28	212.8	16.1	435	25	ABX53761
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31	170.8	12.9	2333	22	AAH74361
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33	159	12.0	215	22	AAH74353
34	130	9.8	338	21	AAH41587
35	128	9.7	562	23	ABV46083
36	106.6	8.1	700	22	AAH74374
37	104.2	7.9	133	24	ABV88907
38	102.8	7.8	203	22	AAH74355
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ALIGNMENTS

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ID AAZ95089 standard; cDNA; 1323 BP.

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XX	21-JUN-2000	(first entry)			
XX	DE	Mouse ATIP coding sequence.			
XX	KW	Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;			
XX	OS	two-hybrid screen; signal transduction; coding sequence.			
XX	Mus sp.				
XX	FR2782084-Al.				
XX	PD	11-FEB-2000.			
XX	PF	04-AUG-1998; 98FR-0009997.			
XX	PR	04-AUG-1998; 98FR-0009997.			
XX	PA	(CNRS) CNRS CENT NAT RECH SCI.			
XX	PI	Elbaz N, Nahmias C, Strosberg AD;			
XX	DR	WPI; 2000-248410/22.			
XX	DR	P-PSDB; AAY83777.			
XX	PT	Nucleic acids coding for angiotensin II receptor AT2 interacting			
XX	PS	proteins useful in screening assays for receptor-protein interaction -			
XX	CC	Claim 1; Page 30-31; 63pp; French.			
XX	CC	This sequence represents the open reading frame (ORF) of the cDNA			
XX	CC	encoding a mouse angiotensin II (AT2) receptor interactive protein			
XX	CC	(ATIP). The gene was isolated from a two-hybrid screen using the			
XX	CC	C-terminal fragment of the mouse AT2 receptor as the "bait" (AAY8378).			
XX	CC	The "target" is a mouse foetal cDNA library. Cells transformed with			
XX	CC	vectors containing the cDNA, or immobilized proteins encoded by it,			
XX	CC	can be used to screen for substances that modulate ATIP-AT2 interaction			
XX	CC	or substances that interact with ATIP, especially using yeast two-			
XX	CC	three-hybrid techniques. Such substances may be useful for treating			
XX	CC	disorders associated with anomalous AT2 receptor signal transduction			
XX	SQ	Sequence 1323 BP; 425 A; 326 C; 325 G; 247 T; 0 other;			
	Query Match	100.0%; Score 1323; DB 21; Length 1323;			
	Best Local Similarity	100.0%; Pred. No. 0;			
	Matches 1323; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1321	TGA 1323	
RESULT 2			
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XX	ID	AAZ99088 standard; cDNA; 1803 BP.	
XX	AC	AAZ99088;	
XX	XX		
DT	21-JUN-2000	(first entry)	
XX	XX		
DE	Mouse	ATIP gene.	
XX	XX		
KW	Mouse;	angiotensin; AT2 receptor interactive protein; ATIP; ss;	
KW	two-hybrid	screen; signal transduction.	
OS	Mus	sp.	
XX	XX		
FH	Key	Location/Qualifiers	
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FT	FT	protein"	
XX	XX		
FN	FR2782084-A1.		
XX	XX		
PD	11-FEB-2000.		

XX 04-AUG-1998; 98FR-0009997.
PF 04-AUG-1998; 98FR-0009997.
PR 04-AUG-1998; 98FR-0009997.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA Elbaz N, Nalmias C, Strosberg AD;
XX P-PSDB; AY83777.
XX WPI: 2000-248410/22.
DR P-PSDB; AY83777.
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
PT proteins useful in screening assays for receptor-protein interaction -
XX Claim 1; Fig 3; 63pp; French.
XX This sequence represents the cDNA encoding a mouse angiotensin II (AT2)
CC receptor interactive protein (ATIP). The gene was isolated from a
CC two-hybrid screen using the C-terminal fragment of the mouse AT2
CC receptor as the "bait" (AY83781). The "target" is a mouse foetal cDNA
CC library. Cells transformed with vectors containing the cDNA, or
CC immobilized proteins encoded by it, can be used to screen for substances
CC that modulate ATIP-AT2 interaction or substances that interact with
CC ATIP, especially using yeast two- or three-hybrid techniques. Such
CC substances may be useful for treating disorders associated with anomalous
CC AT2 receptor signal transduction.
XX
XX Sequence 1803 BP; 539 A; 464 C; 440 G; 360 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 AAAACCCCTCTCTCAAGAACTTGTCTCAGCTCCGCGGAGAGCTAGTGTCTGCTTCAAGGCC 420
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DB 718 TACACCGCAGAGTGTGAGAAAGCTTACAGCAATTTACATTGAGGAGCCAGAAAATATAA 777
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DB 778 ACTCAACTCGAAGAGCGATTTGACAACCTTAAACGCGCGCCCATGAGACCCTTAAGCTTGAG 837
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QY 1201 CTGTGGAAACTGCACAAAGGAGACCTGTGCAGCCCCCAAGAGATCCCAACTCCTCGGCC 1230
DB 1378 CTGTGGAAACTGCACAAAGGAGACCTGTGCAGCCCCCAAGAGATCCCAACTCCTCGGCC 1437
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DB 1438 ATCCCTTTCCAGTCCCCCAGGAATTCGGTTCCTTCTCCAGCCCCCAGCATCTCACCCAGA 1497
QY 1321 TGA 1323
DB 1498 TGA 1500

Search completed: October 21, 2003, 11:11:03
Job time : 259.382 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 270.694 Seconds
(without alignments)
13107.130 Million cell updates sec

Title: US-09-762-194-3
Perfect score: 1323
Sequence: 1 atgtgtgtgtcccaatt.....ccagcatctccacagatga 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

1 865.4 65.4 4937 13 US-10-044-090-76 Sequence 76, Appl
2 644.8 48.7 910 14 US-10-043-487-47 Sequence 47, Appl
3 342.2 25.9 656 10 US-09-764-864-757 Sequence 757, App
4 304.6 23.0 481 10 US-09-764-864-342 Sequence 342, App
5 271.4 20.5 490 11 US-09-918-995-5132 Sequence 5132, App
6 212.8 16.1 435 10 US-09-983-965-3690 Sequence 3690, App
7 159.4 12.0 444 11 US-09-918-995-12481 Sequence 12481, A
8 156.8 11.9 1117 13 US-10-027-632-85144 Sequence 85144, A
9 131.8 10.0 440 11 US-09-918-995-11578 Sequence 11578, A
10 119.6 9.0 464 11 US-09-918-985-5569 Sequence 5569, App
11 104.2 7.9 133 10 US-09-998-598-2218 Sequence 2218, App
12 91.4 6.9 567 9 US-09-925-302-132 Sequence 132, App
13 67 5.1 3489 12 US-10-024-804-1 Sequence 1, Appl
14 55.2 4.2 628 12 US-10-029-386-22859 Sequence 22859, A
15 54.4 4.1 536 12 US-10-029-386-19974 Sequence 19974, A
16 54.4 4.1 599 12 US-10-029-386-6243 Sequence 6243, App
17 54.2 4.1 3269 12 US-10-004-113-7 Sequence 7, Appl
18 51.8 3.9 720 13 US-10-101-487-4 Sequence 76, Appl
19 51.8 3.9 720 13 US-10-101-487-76 Sequence 20733, A
20 50.2 3.8 575 9 US-09-864-761-20733 Sequence 76, Appl
21 50.2 3.8 1969 9 US-09-864-761-3972 Sequence 3972, App
22 49.8 3.8 8895 9 US-09-764-853-887 Sequence 887, App
23 49.8 3.8 8895 9 US-09-764-853-937 Sequence 937, App
24 49.8 3.8 8895 14 US-10-091-438-250 Sequence 250, App
25 49.8 3.8 8895 14 US-10-091-438-256 Sequence 256, App
26 49.8 3.8 9656 9 US-09-764-853-856 Sequence 856, App
27 49.8 3.8 9656 9 US-09-764-853-933 Sequence 933, App
28 49.8 3.8 9656 14 US-10-091-438-246 Sequence 246, App
29 49.8 3.8 9656 14 US-10-091-438-255 Sequence 255, App
30 49.6 3.7 423 9 US-09-864-761-18355 Sequence 18355, A
31 49.4 3.7 475 9 US-09-864-761-6203 Sequence 6203, A
32 49.4 3.7 511 9 US-09-864-761-22817 Sequence 22817, A
33 48.2 3.6 2313 10 US-09-738-973-157 Sequence 157, App
34 48.2 3.6 2313 10 US-09-854-133-157 Sequence 157, App
35 48.2 3.6 2313 14 US-10-144-649A-157 Sequence 157, App
36 48.2 3.6 2314 10 US-09-764-868-12 Sequence 12, Appl
37 48.2 3.6 2802 12 US-10-233-045-35 Sequence 35, Appl
38 47 3.6 3809 13 US-10-001-870-68 Sequence 68, Appl
39 46.6 3.5 541 12 US-10-029-386-12333 Sequence 12333, A
40 46.6 3.5 1040 12 US-10-029-386-26033 Sequence 26033, A
41 46.6 3.5 1371 10 US-09-938-842A-85 Sequence 85, Appl
42 46.2 3.5 700 9 US-09-864-761-17529 Sequence 17529, A
43 46 3.5 6668 12 US-10-311-455-1670 Sequence 1670, App
44 45.8 3.5 272 9 US-09-864-761-18684 Sequence 18684, A
45 45.6 3.4 659158 10 US-09-771-208-20 Sequence 20, Appl

Search completed: October 22, 2003, 03:34:41
Job time : 273.694 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 2085.84 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-3

Perfect score: 1323

Sequence: 1 atgtgtgtgtcccaatt.....ccagcatctaccagatga 1323

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152236056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310.2	99.0	2477	11	AK030510 Mus muscu
2	1292.6	97.7	3963	11	AK031693 Mus muscu
3	982.6	74.3	3237	11	AK035576 Mus muscu
4	896.6	67.8	950	13	BQ921402 AGNCOURT
5	604.4	45.7	657	10	BB628131 BB628131
6	603.2	45.6	1005	13	BQ070423 AGNCOURT
7	595.2	45.0	748	10	BF141309 AGNCOURT
8	592.4	44.7	624	12	BM951991 UI-M-EHO-
9	590.4	44.6	920	13	BQ523654 AGNCOURT
10	579.6	43.8	782	13	BQ702398 UI-M-F10-
11	567.4	42.9	734	14	CB316595 AGNCOURT
12	564.6	42.7	600	13	BQ921755 6093-85 M
13	538.4	40.7	541	4	BX512030 RZPD Mus
14	518.4	39.2	782	9	AU141757 AU141757
15	516.3	39.0	1346	11	BC007328 Homo sapi
16	515.8	39.0	830	9	AU138373 AU138373
17	513.8	38.8	517	10	BF652532 UI-M-AMO-
18	510.6	38.6	530	13	BQ830956 LL6in1027
19	508.6	38.4	710	14	CB723104 UI-M-GHO-
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21	502.8	38.0	509	12	BI319660 lei4a05.Y
22	498.4	37.7	500	9	AA880300 vx39f05.r
23	485.4	36.7	487	10	BF535672 602054069
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25	463.4	35.0	474	9	AA980079 ua28c11.r
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27	451.6	34.1	626	12	BM737916 K-EST006
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29	441.8	33.4	758	10	BQ719490 602690048
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31	435	32.9	732	14	CB246442 UI-M-F10-
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34	418.4	31.6	600	12	BM311947 1964C02.Y
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36	389.6	29.4	862	13	BQ248050 603781419
37	383	28.9	557	10	BE552421 hw26002.x
38	380	28.7	380	10	BE449013 ut85q01.Y
39	380	28.7	573	12	BE536537 393580 MA
40	373.8	28.3	645	13	BQ549647 ik89f06.x
41	369.6	27.9	990	13	BQ893803 AGNCOURT
42	364	27.5	820	13	BQ344537 603522603
43	363.4	27.5	845	9	AU131191 AU131191
44	362.8	27.4	648	10	BB656106 BB656106
45	356.4	26.9	358	9	AI466472 vx39f05.Y

ALIGNMENTS

RESULT 1	AK030510	2477 bp	mRNA	linear	HTC 05-EE -2002
LOCUS	AK030510				
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length cDNA library, clone:530423L05 product:TRANSCRIPTION FACTOR homolog [Homo sapiens], full insert sequence.				
ACCESSION	AK030510				
VERSION	AK030510.1	GI:26326504			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Math. Enzymol. 303, 19-44 (1999)				
MEDLINE	98279263				
PubMed	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PubMed	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PubMed	11076861				
REFERENCE	4				
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staab, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okidori, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,				

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weiss,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

REFERENCE Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 2477)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kuribara,C., Matsuyama,I., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takehashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:ftp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:ftp://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

1. .2477

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/dev stage="adult"

303_-1625

/notes="unnamed protein product; TRANSCRIPTION FACTOR homolog [Homo sapiens] (SPTRIAG33674, evidence: FASTY, 86.1%id, 100%length, match=1317)

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BASE COUNT 709 a 606 c 597 g 565 t

ORIGIN

Query Match 99.0%; Score 1310.2; DB 11; Length 2477;

Best Local Similarity 99.4%; Pred. No. 6.2e-294;

Matches 1315; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 303 ATGCTGTTGTCTCCAAATTCCTTATCCACATCCAGTCCGCTAACCGCAAGGA 362

Qy 61 CTGCTTCAAACTCCGGCTTCCTTGGGGCTCAGGAAAACACTGTCTTCCACACA 120

Db 363 CTGCTTCAAACTCCGGCTTCCTTGGGGCTCAGGAAAACACTGTCTTCCACACA 422

Qy 121 GTTGAAGGGCAGGAGAAATCCAGAGGCTGTGCATCCAGCCAGACAGCTCCA 180

Db 423 GTTGAAGGGCAGGAGAAATCCAGAGGCTGTGCATCCAGCCAGACAGCTCCA 482

Qy 181 GATGTGCTGTCTCCGAGAGAACGCTTGAGTTGGCCCAATACAGACAAAATGTGAAGC 240

Db 483 GATGTGCTGTCTCCGAGAGAACGCTTGAGTTGGCCCAATACAGACAAAATGTGAAGC 542

Qy 241 CAAAGTGGATTCACTCTGCACTCAGGAGCTCTTTCCCGTGGTACACAAAGTTGAA 300

Db 543 CAAAGTGGATTCACTCTGCACTCAGGAGCTCTTTCCCGTGGTACACAAAGTTGAA 602

Qy 301 GCGCTGACAGTTGTGATCCAGCACTCTCTGTCGAGCGGAGAGGAGCTGAAGCAAC 360

Db 603 GCGCTGACAGTTGTGATCCAGCACTCTCTGTCGAGCGGAGAGGAGCTGAAGCAAC 662

Qy 361 AAACCCCTCTCAAGACTTGTGAGCTCCGGGAGAGCTAGTTGCTTCAAGGCC 420

Db 663 AAACCCCTCTCAAGACTTGTGAGCTCCGGGAGAGCTAGTTGCTTCAAGGCC 722

Qy 421 TGTGAGAGCTAGAAAAGGCTAGGCTGACTTACAGACAGGCTATCAAGATTTGTCCAG 480

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ORGANISM Mus musculus
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1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new genes
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20499374
11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagacka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,I., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishi.Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,J., Ring,B., Ringwald,M., Rodriguez,L., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seva,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyochika,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
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 Nature 409 (6821), 685-690 (2001)
 21085660
 11217851
 5
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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 6 (bases 1 to 3963)
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 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
 URL:http://fantom.gsc.riken.go.jp/.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REFERENCE 1 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Cloning and characterization of M1SG1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1323)
AUTHORS Seibold,S., Wanner,C. and Galle,J.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Department of Medicine, University of
Wuerzburg, Josef Schneider Str 2, Wuerzburg 97080, Germany

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REFERENCE 1 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Molecular characterization of ATIP, a novel angiotensin II type 2
receptor-interacting protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1803)
AUTHORS Elbaz,N., Strosberg,A.D. and Nahmias,C.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1999) Institut Cochin de Genetique Moleculaire,
CNRS UPR415, 22, rue Mechain, Paris 75014, France
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 BC043321
 LOCUS
 DEFINITION
 MGC:49379 IMAGE:5366361, complete cds.
 ACCESSION
 BC043321
 VERSION
 BC043321.1 GI:27694046

KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 3629)
 AUTHORS
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,i K.,
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 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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 Carninci,P., Prange,C., Raha,S.S., Iqballano,N.A., Peters,G.J.,
 Abramson,R.D., Mullen,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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 2388257
 MEDLINE
 PUBMED
 12477932
 REFERENCE
 2 (bases 1 to 3629)
 AUTHORS
 Strausberg,R.
 Direct Submission
 TITLE
 Submitted (09-JUN-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Steven
 Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jacqueline
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.lln.gov>
 Series: IRAC Plate: 86 Row: n Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES
source

Location/Qualifiers
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Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
BC041777

LOCUS BC041777 5218 bp mRNA linear ROD 10-JUN-2003
DEFINITION Mus musculus expressed sequence A1481402, mRNA (cDNA clone
MGC:31380 IMAGE:4240274), complete cds.

ACCESSION BC041777
VERSION BC041777.1 GI:27469800
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 5218)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Carroll, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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TITLE
JOURNAL
MEDLINE
PUBMED
12477932

REFERENCE 2 (bases 1 to 5218)
Strausberg, R.

AUTHORS
TITLE
JOURNAL
Submitted (23-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mge.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAC Plate: 43 Row: 0 Column: 3.

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gene

CDS

BASE COUNT 1591 a 1192 c 1183 g 1262 t
ORIGIN
Query Match 100.0%; Score 354; DB 10; Length 5218;
Best Local Similarity 100.0%; Fred. No. 2.3e-78;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATCAGACAGACCGGAGACTGGAGACCGGCTGAGGACTTATACACGAGAGTGT 60
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RESULT 5

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MGC:49685 IMAGE:4240274, complete cds.

DEFINITION

BC042206

ACCESSION

BC042206.1 GI:27503397

VERSION

MGC.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 5219)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Generation and initial analysis of more than 15,000 full-length

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22388257

12477932
2 (bases 1 to 5219)
Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Maduro, Q.J., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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Young, A., Zhang, L.-H. and Green, E.D.

Cloned from: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
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12477932
2 (bases 1 to 5219)
Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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NIH-MGC Project URL: <http://mgc.nci.nih.gov>
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Tissue Procurement: Jeffrey E. Green, M.D.
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Sequencing Center (NISC),
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Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
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12477932
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Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
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/clone_lib="NCI CGAP_Kid14"
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1. .5219
/gene="AI481402"
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RYTEII SYPTNPFNIIKAKVLSRVLPQZISVMKDTNPQVTCGSSPSPGSKLITM
MNAFRSDFKAGKAEIPIPNKTHKQFNKLITSQAQVTHSNVASLIGVPRITSAKS

12477932
2 (bases 1 to 5219)
Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.J., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Cloned from: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAC Plate: 85 Row: i Column: 19.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="MGC:49685 IMAGE:4240274"
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/clone_lib="NCI CGAP_Kid14"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. .5219
/gene="AI481402"
/db_xref="LocusID:102103"
/db_xref="MGI:2142572"
53. .2707
/codon_start=1
/product="AI481402 protein"
/protein_id="AAH42206.1"
/db_xref="GI:27503398"
/db_xref="LocusID:102103"
/translation="MGQMLRGTLPNGHVDGECFVLPAPFKSRTRVLGSECKVTWTFD
PHLDHNDSDIQSSTELTLSVSGQSGSYEMGWGNGGAICTDKAGCMSTPVROP
PNLSFRLEPAEVKYNVNGPRDKAPNLKGPINMKNLGSNTKNTATVGSKV
RYTEII SYPTNPFNIIKAKVLSRVLPQZISVMKDTNPQVTCGSSPSPGSKLITM
MNAFRSDFKAGKAEIPIPNKTHKQFNKLITSQAQVTHSNVASLIGVPRITSAKS

12477932
2 (bases 1 to 5219)
Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.J., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Cloned from: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAC Plate: 85 Row: i Column: 19.
Location/Qualifiers
1. .5219
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="MGC:49685 IMAGE:4240274"
/tissue_type="Kidney, normal. 5 month old male mouse."
/clone_lib="NCI CGAP_Kid14"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. .5219
/gene="AI481402"
/db_xref="LocusID:102103"
/db_xref="MGI:2142572"
53. .2707
/codon_start=1
/product="AI481402 protein"
/protein_id="AAH42206.1"
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RYTEII SYPTNPFNIIKAKVLSRVLPQZISVMKDTNPQVTCGSSPSPGSKLITM
MNAFRSDFKAGKAEIPIPNKTHKQFNKLITSQAQVTHSNVASLIGVPRITSAKS

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:19 ; Search time 68.0658 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-08-762-194-5

Perfect score: 354

Sequence: 1 catcagacagaccgacgca.....atgcttttaacgaagggtg 354

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
- 25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	354	100.0	354	21	Mouse ATIP coding
2	354	100.0	1323	21	Mouse ATIP coding
3	354	100.0	1803	21	Mouse ATIP gene.
4	246.8	69.7	481	22	Human cDNA encoding
5	246.8	69.7	481	25	Human novel polynu
6	246.8	69.7	910	24	Human cDNA encoding
7	246.8	69.7	1615	24	Polynucleotide enc
8	246.8	69.7	1758	22	Nucleotide sequenc
9	246.8	69.7	3315	22	Human cDNA sequenc
10	246.8	69.7	3654	22	Human cDNA sequenc
11	246.8	69.7	3807	25	Human cDNA encodin
12	246.8	69.7	4937	25	Human cDNA #76 dif
13	246.8	69.7	5961	22	Nucleotide sequenc
14	245.2	69.3	1191	22	Nucleotide sequenc
15	245.2	69.3	1369	22	Nucleotide sequenc
16	245.2	69.3	1458	22	Nucleotide sequenc
17	245.2	69.3	5799	22	Nucleotide sequenc
18	234	66.1	656	22	Human cDNA encodin
19	234	66.1	656	25	Human novel polynu
20	232.4	65.6	1308	21	Human ATIP coding
21	232.4	65.6	3742	21	Human ATIP gene.
22	232.4	65.6	3742	22	Nucleotide sequenc
23	225.4	63.7	830	22	Human cDNA clone (
24	160.2	45.3	242	25	Human cDNA sequenc
25	154.4	43.6	775	22	Nucleotide sequenc
26	130	36.7	338	21	Human secreted exp
27	128	36.2	562	23	Human prostate exp
28	104.2	29.4	133	24	Human colon cancer
29	96	27.1	791	25	Human genomic DNA
30	96	27.1	3287	21	Human secreted pro
31	85	24.0	600	22	Nucleotide sequenc
32	82	23.2	106	22	Nucleotide sequenc
33	72.2	20.4	700	22	Nucleotide sequenc
34	71.6	20.2	4184	25	Novel human cDNA s
35	70.2	19.8	203	22	Nucleotide sequenc
36	53	15.0	435	22	Nucleotide sequenc
37	50.8	14.4	540	23	Human prostate exp
38	50	14.1	74	22	Nucleotide sequenc
39	45.2	12.8	458	22	Nucleotide sequenc
40	44.6	12.6	1080	24	Mouse ischaemic co
41	43.6	12.3	1563	24	Nucleotide sequenc
42	43	12.1	96	22	Nucleotide sequenc
43	42.2	11.9	843	23	DNA encoding novel
44	42	11.9	240	23	Drosophila melanog
45	42	11.9	2240	23	Drosophila melanog

ALIGNMENTS

RESULT 3
AAZ99088
ID AAZ99088 standard; cDNA; 1803 BP.

DT 21-JUN-200

KW Mouse: angiotensin

US Mus sp. XX

Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1. *What is the main purpose of the study?*

Journal of Management Inquiry

||||| 853 TGGGAGAGTGGAAATGCTGAAGAGACCTATGAACCTCCCTTTTCAGAAATCAAGAAG 912
QY 241 AGCCATGAGATGGAGAGAGTCACTGGAGGATCTGCTTAATGAGAGCGAGGAATCGCTG 300
Db 913 AGCCATGAGATGGAGAGAGTCACTGGAGGATCTGCTTAATGAGAGCGAGGAATCGCTG 972
QY 301 GAGAAACAATCAATGATCTGAAGAGTGAAGACGATGCTTTAAACGAAAGGTTG 354
Db 973 GAGAAACAATCAATGATCTGAAGAGTGAAGACGATGCTTTAAACGAAAGGTTG 1026

Search completed: October 21, 2003, 11:11:04
Job time : 69.0658 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 72.4306 Seconds
(without alignments)
13107.130 Million cell updates sec

Title: US-09-762-194-5
Perfect score: 354
Sequence: 1 catcacagacagcggacgga.....atgctttaacgaaaggttg 354

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1 246.8 69.7 481 10 US-09-764-864-342
2 246.8 69.7 910 14 US-10-043-487-47
3 246.8 69.7 4937 13 US-10-044-090-76
4 234 66.1 656 10 US-09-764-864-757
5 194.8 55.0 490 11 US-09-918-995-3132
6 104.2 29.4 133 10 US-09-998-598-2218
7 43 12.1 32069 12 US-10-004-113-7
c 8 42.2 11.9 536 12 US-10-029-386-19974
9 42.2 11.9 599 12 US-10-029-386-6243
10 40.8 11.5 253 10 US-09-960-352-6844
11 39.4 11.1 315 9 US-09-864-761-21723
12 38.6 10.9 461 10 US-09-960-352-945
c 13 38.2 10.8 475 9 US-09-864-761-6203
c 14 38.2 10.8 511 9 US-09-864-761-22817
15 37.8 10.7 1607 10 US-09-917-600A-497
c 16 37.6 10.6 496 9 US-09-864-761-2534
c 17 37.4 10.6 232 9 US-09-864-761-19928
18 37 10.5 1460 10 US-09-822-830A-504
19 37 10.5 1560 10 US-09-880-107-2410
20 37 10.5 1560 12 US-10-096-534-29
21 37 10.5 1560 14 US-10-146-473-30
22 37 10.5 2309 12 US-10-269-909-52
23 37 10.5 2309 12 US-10-269-909-53
24 37 10.5 2309 12 US-10-269-909-54
25 37 10.5 2309 12 US-10-269-909-55
26 37 10.5 2309 12 US-10-269-909-56
27 37 10.5 4201 9 US-09-925-301-478
28 37 10.5 4201 14 US-10-106-698-343
29 37 10.5 4252 11 US-09-919-039-334
30 36.8 10.4 1546 12 US-10-067-279-3
31 36.8 10.4 1680 12 US-10-067-279-8
32 36.6 10.3 551 12 US-10-029-386-5590
33 36.6 10.3 3809 13 US-10-001-870-68
34 36 10.2 3489 12 US-10-294-804-1
c 35 36 10.2 143899 11 US-09-972-546-15
36 35.8 10.1 477 11 US-09-918-995-22506
c 37 35.8 10.1 663 13 US-10-027-632-213131
c 38 35.8 10.1 663 13 US-10-027-632-213132
39 35.8 10.1 1631 14 US-10-103-313-169
40 35.8 10.1 1882 14 US-10-103-313-280
c 41 35.6 10.1 305 9 US-09-864-761-19262
c 42 35.6 10.1 474 9 US-09-864-761-11284
c 43 35.4 10.0 360 9 US-09-864-761-28274
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45 35.4 10.0 700 9 US-09-864-761-17529

Search completed: October 21, 2003, 21:04:07
Job time : 560.115 secs

Sequence 342, App
Sequence 47, Appl
Sequence 76, Appl
Sequence 757, App
Sequence 5132, Ap
Sequence 2218, Ap
Sequence 7, Appli
Sequence 19974, A
Sequence 6243, Ap
Sequence 6844, Ap
Sequence 21723, A
Sequence 945, App
Sequence 6203, Ap
Sequence 22817, A
Sequence 497, App
Sequence 2534, Ap
Sequence 19928, A
Sequence 504, App
Sequence 2410, Ap
Sequence 29, Appl
Sequence 30, Appl
Sequence 52, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 478, App
Sequence 343, App
Sequence 334, App
Sequence 3, Appli
Sequence 8, Appli
Sequence 5590, Ap
Sequence 68, Appl
Sequence 1, Appli
Sequence 15, Appl
Sequence 22506, A
Sequence 213131,
Sequence 213132,
Sequence 169, App
Sequence 280, App
Sequence 19262, A
Sequence 11284, A
Sequence 28274, A
Sequence 11696, A
Sequence 17529, A

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 9570.68 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-7
Perfect score: 3742
Sequence: 1 cagtgatgtgttcagag,.....aaaaaaaaaaaaaaaaaaaa 3742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*

28: em.un:*
29: em.vi:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
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34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.man:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3742	100.0	3742	6	AX210037	Sequence	AX210037 Sequence
2	3407	91.0	3455	9	AF121259	Homo sapi	AF121259 Homo sapi
3	3282	87.7	5214	9	HSME00681	Homo sapi	AL096842 Homo sapi
4	3268.2	87.3	5799	6	AX210061	Sequence	AX210061 Sequence
5	3268.2	87.3	5857	9	AB033114	Homo sapi	AB033114 Homo sapi
6	3267	87.3	3315	6	BD160624	Primer fo	BD160624 Primer fo
7	3267	87.3	3315	9	AK024357	Homo sapi	AK024357 Homo sapi
8	2841.2	75.9	2895	9	BC033842	Homo sapi	BC033842 Homo sapi
9	2519.2	67.3	2348	9	AK000172	Homo sapi	AK000172 Homo sapi
c 10	2314.8	61.9	100000	9	AB020864	Homo sapi	AB020864 Homo sapi
11	2314.8	61.9	131299	9	AF165145	Homo sapi	AF165145 Homo sapi
12	2313.2	61.8	2850	6	AX210056	Sequence	AX210056 Sequence
13	2313.2	61.8	171075	2	AC026842	Homo sapi	AC026842 Homo sapi
14	2305.8	61.6	2333	6	AX210036	Sequence	AX210036 Sequence
c 15	2297.6	61.4	174025	9	AC124069	Homo sapi	AC124069 Homo sapi
c 16	2159.8	57.7	195290	9	AP006249	Homo sapi	AP006249 Homo sapi
c 17	2126.2	56.8	28067	9	AP006251	Homo sapi	AP006251 Homo sapi
18	1937	51.8	1970	9	AF394227	Homo sapi	AF394227 Homo sapi
19	1937	51.8	1977	9	AF293357	Homo sapi	AF293357 Homo sapi
20	1890.2	50.5	1927	9	AK026661	Homo sapi	AK026661 Homo sapi
21	1594.2	42.6	1615	6	AX301208	Sequence	AX301208 Sequence
22	1229.8	32.9	5218	10	BC041777	Mus musc.	BC041777 Mus musc.
23	1226.4	32.8	3629	10	BC043321	Mus musc.	BC043321 Mus musc.
24	1225.2	32.7	5219	10	BC042206	Mus musc.	BC042206 Mus musc.
25	1177.4	31.5	1758	6	AX209989	Sequence	AX209989 Sequence
26	1177.4	31.5	3654	6	AX209987	Sequence	AX209987 Sequence
27	1177.4	31.5	3813	6	AX210064	Sequence	AX210064 Sequence
28	1175.8	31.4	1459	6	AX209991	Sequence	AX209991 Sequence
29	1173.4	31.4	1191	6	AX209993	Sequence	AX209993 Sequence
30	1118	29.9	1142	9	BC017740	Homo sapi	BC017740 Homo sapi
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35 740 19.8 830 6 BD149938 Primer fo
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37 658.8 17.6 888 6 BD018043
38 658.8 17.6 888 6 BD097981
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44 489.4 13.1 729 9 HUNZB67D11
45 483.8 12.9 505 6 BD154906

ALIGNMENTS

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DEFINITION Sequence 53 from Patent WO0157209.
ACCESSION AX210037
VERSION AX210037.1 GI:15424423
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Nahmias,C., Strosberg,A.D. and Nouet,S.
TITLE Novel family of proteins, called atip, nucleic sequences coding for same and uses thereof
JOURNAL Patent: WO 0157209-A 53 09-AUG-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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SUMMARIES

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5	3250.6	86.9	5799	22	AAH74383 Nucleotide sequenc
6	3249	86.8	5961	22	AAH74385 Nucleotide sequenc
7	2473.4	66.1	3287	21	AAH74380 Human secreted pro
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9	2305.8	61.6	2333	22	AAH74361 Nucleotide sequenc
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11	1594.2	42.6	1615	24	AAH99905 Polynucleotide enc
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ALIGNMENTS

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AC AAZ99091;
XX 21-JUN-2000 (first entry)
XX Human ATIP gene.
XX Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
XX two-hybrid screen; signal transduction; human.
OS Homo sapiens.
FH Key Location/Qualifiers
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FT /note= "angiotensin II (AT2) receptor interactive
protein"
XX FR2782084-A1.
XX 11-FEB-2000.
XX 04-AUG-1996; 98FR-0009997.
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XX (CNRS) CNRS CENT NAT RECH SCI.
XX Elbaz N, Nahmias C, Strosberg AD;
XX WFI; 2000-248410/22.
XX P-PSDB; AAY83780.
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
XX proteins useful in screening assays for receptor-protein interaction -
XX Claim 1; Fig 4; 63pp; French.
XX This sequence represents the cDNA encoding a human angiotensin II (AT2)
XX receptor interactive protein (ATIP). The gene was isolated using a
XX fragment of the mouse gene (AAZ99088). Cells transformed with vectors
XX containing the cDNA, or immobilized proteins encoded by it, can be used
XX to screen for substances that modulate ATIP-AT2 interaction or
XX substances that interact with ATIP, especially using yeast two- or
XX three-hybrid techniques. Such substances may be useful for treating
XX disorders associated with anomalous AT2 receptor signal transduction.
XX Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;
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Db 2581 CTTTTCCTCCACCATTCAGAGGCAAAAAGCAAACTTCTACCTCTACCTTACTTCTTCTC 2640
QY 2641 GGGCAAGGATAAAGGAATATGATTTTCCAGAGCCCAAGAGGCAAGCTCATCTCCAGT 2700
Db 2641 GGGCAAGGATAAAGGAATATGATTTTCCAGAGCCCAAGAGGCAAGCTCATCTCCAGT 2700
QY 2701 CTGAAACCACTTTCCAAAATAAAGCTGATTTTGAATATTAATAATTTGGAAAA 2760
Db 2701 CTGAAACCACTTTCCAAAATAAAGCTGATTTTGAATATTAATAATTTGGAAAA 2760
QY 2761 TTAGATAAAGAGCAGAGGAGTCAATGGCTAGTATTAATTAAGAGGTAGGAT 2820
Db 2761 TTAGATAAAGAGCAGAGGAGTCAATGGCTAGTATTAATTAAGAGGTAGGAT 2820
QY 2821 CAGTGGTTACCGATGATGCACTCTGATAGAAGAAAAACAGTCTGGAGGATAGGCTCA 2880
Db 2821 CAGTGGTTACCGATGATGCACTCTGATAGAAGAAAAACAGTCTGGAGGATAGGCTCA 2880
QY 2881 ITTTTCAGTTACCCCTTAAGGAGTCCCTTTGTCTTTGGAAAAAGTACAGAAATGGTCCGCT 2940
Db 2881 ITTTTCAGTTACCCCTTAAGGAGTCCCTTTGTCTTTGGAAAAAGTACAGAAATGGTCCGCT 2940
QY 2941 ICTTTCCCATGAGTGGAAAAATGTGGCTTGTCCACTCTCTCCAGTTTGCATTTCACTT 3000
Db 2941 ICTTTCCCATGAGTGGAAAAATGTGGCTTGTCCACTCTCTCCAGTTTGCATTTCACTT 3000
QY 3001 CTTTCCAAAACTTTATTACCTTCCCTTAACTGAGACTTTGAAAAAGSTGGAGGAAAC 3060
Db 3001 CTTTCCAAAACTTTATTACCTTCCCTTAACTGAGACTTTGAAAAAGSTGGAGGAAAC 3060
QY 3061 TGTGCTTTATCTCCCTCCCTCCCTGCACTGTCACTTGTGATGTCACTATTTTACTAATC 3120
Db 3061 TGTGCTTTATCTCCCTCCCTCCCTGCACTGTCACTTGTGATGTCACTATTTTACTAATC 3120
QY 3121 TACATTCAGTGGCTGTACAAATAACAGCTGTAGTAAGAAGAGATTACGGATGCTAGAGT 3180
Db 3121 TACATTCAGTGGCTGTACAAATAACAGCTGTAGTAAGAAGAGATTACGGATGCTAGAGT 3180
QY 3181 GATATTTGGTCAATTTACATGTAAGTACATAGCAAGTGTGATCACTGATGTTTC 3240
Db 3181 GATATTTGGTCAATTTACATGTAAGTACATAGCAAGTGTGATCACTGATGTTTC 3240
QY 3241 TTTTAAATTAAGTATTTTGTGTTTAAAGTCTTTAACTTCCATCTTCATCATGTATGT 3300
Db 3241 TTTTAAATTAAGTATTTTGTGTTTAAAGTCTTTAACTTCCATCTTCATCATGTATGT 3300
QY 3301 ACCTTCCATGTTTGGCTTCTGATTAATGGAAATGTAGGTTCACTGCCACTTCATGAGATA 3360
Db 3301 ACCTTCCATGTTTGGCTTCTGATTAATGGAAATGTAGGTTCACTGCCACTTCATGAGATA 3360
QY 3361 CTCTGCTCAGCTTCCAAAGTGTGTTCTCAATGACATAGCAAAAGTGGTTGGCAATTC 3420
Db 3361 CTCTGCTCAGCTTCCAAAGTGTGTTCTCAATGACATAGCAAAAGTGGTTGGCAATTC 3420

XX	WPI: 2001-48880/53.
DR	P-PSDE; AAG63540.
DR	
XX	New protein family, designated hATP, which interacts with the ATP
XX	receptor of angiotensin II are anti-oncogenic and useful to detect and
XX	treat cancer or precancerous conditions -
XX	Claim 11; Page 106-109; 118pp; French.
XX	
XX	The present sequence encodes an isoform of the human ATP protein,
CC	designated hATP1. ATP has isoforms designated hATP2, hATP3, hATP4,
CC	hATP5 and hATP6. All ATP proteins comprise in their C-terminals
CC	a common fragment which interacts with the angiotensin II (AT2)
CC	receptor. ATP proteins have antioncogenic functions. The human ATP
CC	gene has 17 exons, and is located at chromosome region 8p21.3-p22.
CC	ATP polynucleotides and polypeptides are used to detect, evaluate or
CC	give prognosis for a cancer or pre-cancer condition, and as an
CC	anti-tumour medicament.
XX	
SQ	Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;
	Query Match 100.08; Score 3742; DB 22; Length 3742;
	Best Local Similarity 100.04; Pred. No. 0;
	Matches 3742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CAGTGTGATGTGTTTCAGAGCGAGCTTTAGAGCTTCAGAGAGGAGATTGATTCAGAGS 60
Db	1 CAGTGTGATGTGTTTCAGAGCGAGCTTTAGAGCTTCAGAGAGGAGATTGATTCAGAGS 60
Qy	61 AAGAGCATCATTTGGCAACATCTGAAAGTGAAACGGAGACACATCTGGCGAG 120
Db	61 AAGAGCATCATTTGGCAACATCTGAAAGTGAAACGGAGACACATCTGGCGAG 120
Qy	121 CCTGGGGAGATTTTCTCTATCGCTCTGTGTGGATGACATTTGCTGTGTAGGCAT 180
Db	121 CCTGGGGAGATTTTCTCTATCGCTCTGTGTGGATGACATTTGCTGTGTAGGCAT 180
Qy	181 TTTCCCTCTGACTGTATTTCTGGCCCTTGAAGAGTACTGAGTTTAAAGACAGATGTGA 240
Db	181 TTTCCCTCTGACTGTATTTCTGGCCCTTGAAGAGTACTGAGTTTAAAGACAGATGTGA 240
Qy	241 CAGTCCATGGAATTGGCTCTTCTGTGAATCTGGCCACTGCTCCGAGACATGTGTT 300
Db	241 CAGTCCATGGAATTGGCTCTTCTGTGAATCTGGCCACTGCTCCGAGACATGTGTT 300
Qy	301 GTCTCCCAATTCCTTATCCACCATTCACATACGACTGAGGCCCAAGAGATTGCTTGG 360
Db	301 GTCTCCCAATTCCTTATCCACCATTCACATACGACTGAGGCCCAAGAGATTGCTTGG 360
Qy	361 AAACCTTCGACTTCCTTCAGGGTTTAGAGAGACATCTGTTGTTTTCCACACAGTTGAAA 420
Db	361 AAACCTTCGACTTCCTTCAGGGTTTAGAGAGACATCTGTTGTTTTCCACACAGTTGAAA 420
Qy	421 GAGCAGGCAAAAGATCCTCGAAGCTATGTATCCAGCCACACAGACGCTCCGATGGCT 480
Db	421 GAGCAGGCAAAAGATCCTCGAAGCTATGTATCCAGCCACACAGACGCTCCGATGGCT 480

Qy	1321	GAAGGTTTCAGACGAGGAGTGAAGAAATGAAAGCTGGATGAACTGGACAGCACTGGCA	1330
Db	1321	GAAGGTTTCAGACGAGGAGTGAAGAAATGAAAGCTGGATGGAACAGACATGGCA	1330
Qy	1381	CTCAAGGAGCTTTCCACGGCAGGAGCTGTCTGCAAGAGTGCCTGGAGAGAGTGG	1440
Db	1381	CTCAAGGAGCTTTCCACGGCAGGAGCTGTCTGCAAGAGTGCCTGGAGAGAGTGG	1440
Qy	1441	AGTCACACCGGACTCTCTATGGAAACAGAGAGCTTCTGTGGAAACTGCACAAATGGGA	1500
Db	1441	AGTCACACCGGACTCTCTATGGAAACAGAGAGCTTCTGTGGAAACTGCACAAATGGGA	1500
Qy	1501	CGTGTGAGCCCAAGAGATCCCGACATCTCTCGGCCCATCCCTTTCGAGTCAACCAAG	1560
Db	1501	CGTGTGAGCCCAAGAGATCCCGACATCTCTCGGCCCATCCCTTTCGAGTCAACCAAG	1560
Qy	1561	TTCGGGCTCGTTCCTAGCCCGACATTTCAACCGAGTGAACCTGCCAAGTCCACAG	1620
Db	1561	TTCGGGCTCGTTCCTAGCCCGACATTTCAACCGAGTGAACCTGCCAAGTCCACAG	1620
Qy	1621	ACTCTCTGAAAGCATTTTATGTCAGAGTCTGAGAGCTGACCCCAAGAGAGAGTGGGA	1680
Db	1621	ACTCTCTGAAAGCATTTTATGTCAGAGTCTGAGAGCTGACCCCAAGAGAGAGTGGGA	1680
Qy	1681	CAAGAGTATATCAGACACAGTGTGATCATCCTAGTGTAACTGGAGGTCACCAACCGGG	1740
Db	1681	CAAGAGTATATCAGACACAGTGTGATCATCCTAGTGTAACTGGAGGTCACCAACCGGG	1740
Qy	1741	AATCGAGCTCTTGAGACTGAAAGTCTGGAGAGAGACTTTTGCTCGTCCAAAAGATCC	1800
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Qy	1801	TCGAAAAAGAGTTTAAAAAAGATTTCCGCACTGACACGAGAGCTTTGTTGCACAAAGAC	1860
Db	1801	TCGAAAAAAGATTTAAAAAAGATTTCCGCACTGACACGAGAGCTTTGTTGCACAAAGAC	1860
Qy	1861	TTAAGAAGCAGAGACTTTGTTCAATGCGCTTTTCACTAAGCAATAGGGGAAAACTC	1920
Db	1861	TTAAGAAGCAGAGACTTTGTTCAATGCGCTTTTCACTAAGCAATAGGGGAAAACTC	1920
Qy	1921	TCAGGGCCCTATTAGAGTTATTAACCTTTGTATGTTCTTCAACAGACACCTCTTG	1980
Db	1921	TCAGGGCCCTATTAGAGTTATTAACCTTTGTATGTTCTTCAACAGACACCTCTTG	1980
Qy	1981	GAGTTTTCAGTCTGACTGTGGGGTGGGGGTGTGAATGAAATGATGTCAACAGAGTGT	2040
Db	1981	GAGTTTTCAGTCTGACTGTGGGGTGGGGGTGTGAATGAAATGATGTCAACAGAGTGT	2040
Qy	2041	ATGTGTCTGATGCAAGCTCGTCTGCTGTGTATTAATGTCAAAATCTGAATATCTG	2100
Db	2041	ATGTGTCTGATGCAAGCTCGTCTGCTGTGTATTAATGTCAAAATCTGAATATCTG	2100
Qy	2101	TATGTACTAATCAAAATAATCAATCAATCAGCAATATACATTTTCAGCCAAAGCATA	2160
Db	2101	TATGTACTAATCAAAATAATCAATCAATCAGCAATATACATTTTCAGCCAAAGCATA	2160
Qy	2161	AGAAAAAGCAATAGTCTGTTGAAATTATGATCACTACCAACCACTGTCTCAGAGCTGT	2220

Search completed: October 21, 2003, 11:11:12
Job time : 727.498 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 765.637 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-7
Perfect score: 3742
Sequence: 1 cagtggtggtggttcagag.....aaaaaaaaaaaaaaaaaaaaa 3742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/US07_PUB_PUB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description

1	3251.6	86.9	4937	13	US-10-044-090-76	Sequence 76, Appl
2	894	23.9	910	14	US-10-043-487-47	Sequence 47, Appl
c 3	519.2	13.9	581	14	US-10-106-698-125	Sequence 125, Appl
4	509.2	13.6	656	10	US-09-764-864-757	Sequence 757, App
5	449.6	12.0	481	10	US-09-764-864-342	Sequence 342, App
6	412	11.0	464	11	US-09-918-995-5569	Sequence 5569, Ap
7	405.4	10.8	490	11	US-09-918-995-5132	Sequence 5132, App
c 8	366	9.8	366	10	US-09-964-844A-352	Sequence 352, App
c 9	366	9.8	366	10	US-09-880-107-1238	Sequence 1238, Ap
10	215.8	5.8	444	11	US-09-918-995-12481	Sequence 12481, A
11	212.8	5.7	435	10	US-09-983-965-3690	Sequence 3690, Ap
12	209.6	5.6	1117	13	US-10-027-632-85144	Sequence 85144, A
13	133	3.1	133	10	US-09-998-598-2218	Sequence 2218, Ap
14	117.8	3.1	440	11	US-09-918-995-11578	Sequence 11578, A
15	93.6	2.5	567	9	US-09-925-302-132	Sequence 132, App
16	71	1.9	313	10	US-09-983-965-2834	Sequence 2834, Ap
c 17	63.4	1.7	14006	12	US-10-311-455-1931	Sequence 1931, Ap
18	60	1.6	60	12	US-09-908-975-10969	Sequence 10969, A
c 19	56.8	1.5	9539	12	US-10-240-453-54	Sequence 54, Appl
c 20	56.8	1.5	9539	14	US-10-239-676-52	Sequence 52, Appl
c 21	55.6	1.5	6668	12	US-10-311-455-1670	Sequence 1670, Ap
c 22	55.6	1.5	7657	12	US-10-311-455-1995	Sequence 1995, Ap
c 23	55.6	1.5	7657	14	US-10-239-676-185	Sequence 185, App
24	54.6	1.5	554	13	US-10-101-467-106	Sequence 106, App
25	53.2	1.4	650	13	US-10-027-632-320324	Sequence 320324,
c 26	53.2	1.4	3673778	12	US-10-312-841-2	Sequence 2, Appli
27	52.8	1.4	522	13	US-10-101-487-71	Sequence 71, Appl
c 28	52.8	1.4	530	13	US-10-101-487-73	Sequence 73, Appl
c 29	52.8	1.4	534	13	US-10-101-487-69	Sequence 69, Appl
c 30	52.6	1.4	6334	12	US-10-311-455-1186	Sequence 1186, Ap
c 31	52.4	1.4	410	12	US-09-814-353-4678	Sequence 4678, Ap
c 32	52.4	1.4	410	12	US-09-814-353-10977	Sequence 10977, A
33	52.2	1.4	1528	13	US-10-027-632-39070	Sequence 39070, A
34	52.2	1.4	1528	13	US-10-027-632-83911	Sequence 83911, A
c 35	52.2	1.4	10369	12	US-10-311-455-365	Sequence 365, App
c 36	52	1.4	7571	12	US-10-311-455-500	Sequence 500, App
c 37	52	1.4	17934	12	US-10-311-455-1692	Sequence 1692, Ap
c 38	51.8	1.4	6944	14	US-10-172-086-112	Sequence 112, App
c 39	51.8	1.4	113515	12	US-10-311-455-2147	Sequence 2147, Ap
c 40	51.6	1.4	529	10	US-09-983-965-2109	Sequence 2109, Ap
c 41	51.6	1.4	11670	12	US-10-240-452-25	Sequence 25, Appl
c 42	51.4	1.4	442	10	US-09-960-352-12911	Sequence 129.1, A
c 43	51.2	1.4	659158	10	US-09-771-208-20	Sequence 20, Appl
44	51	1.4	268	10	US-09-960-352-11467	Sequence 11467, A
45	50.8	1.4	3489	12	US-10-294-804-1	Sequence 1, Appli

Search completed: October 22, 2003, 03:34:47
Job time : 770.637 secs

OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 09:08:27 ; Search time 5899.62 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-7
Sequence: 1 cagtggtgtgttgcagag.....aaaaaaaaaaaaaaaaaaaaa 3742
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
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27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1338.8	35.8	3963	11	AK031693	AK031693 Mus muscu
2	1191.6	31.8	2477	11	AK030510	AK030510 Mus muscu
c 3	1074.8	28.7	1130	9	AL574093	AL574093 AL574093
4	1051	28.1	3237	11	AK035576	AK035576 Mus muscu
5	1014.4	27.1	1127	9	AL550130	AL550130 AL550130
c 6	1005	26.9	1201	9	AL528732	AL528732 AL528732
7	986.4	26.4	1201	9	AL528733	AL528733 AL528733
c 8	952.4	25.5	1070	13	BX394445	BX394445 BX394445
9	868.8	23.2	1005	13	BQ070423	BQ070423 AGNCOURT
c 10	847.6	22.7	908	13	BX415760	BX415760 BX415760
11	780.4	20.9	794	10	BG742834	BG742834 602632568
12	765.4	20.5	835	9	AU119683	AU119683 AU119683
13	761.8	20.4	845	9	AU131191	AU131191 AU131191
14	751.4	20.1	990	13	BQ893803	BQ893803 AGNCOURT
15	740	19.8	830	9	AU138373	AU138373 AU138373
16	738	19.7	776	12	BM716134	BM716134 UI-E-CKI-
17	734.8	19.6	920	13	BU172503	BU172503 AGNCOURT
18	728.2	19.5	1346	11	BC007328	BC007328 Homo sapi
19	716.6	19.2	867	10	BG676152	BG676152 602622551
c 20	714	19.1	716	13	BU685931	BU685931 UI-CF-DU1
21	708.6	18.9	785	13	BU940431	BU940431 AGNCOURT
22	703.6	18.8	785	9	AU134834	AU134834 AU134834
23	701.6	18.7	782	9	AU141757	AU141757 UI-CF-FNO
c 24	696.6	18.6	715	13	BU609177	BU609177 UI-CF-FNO
25	691	18.5	747	9	AU138331	AU138331 AU138331
26	681.4	18.2	707	10	BG696701	BG696701 602639717
c 27	681	18.2	690	12	BM665224	BM665224 UI-E-CKI-
28	675	18.0	874	13	BU151347	BU151347 AGNCOURT
29	672.4	18.0	676	12	BM702509	BM702509 UI-E-CKI-
c 30	670.4	17.9	684	13	BU686234	BU686234 UI-CK-DU1
31	662.4	17.7	728	10	BF965779	BF965779 60227408
c 32	661.4	17.7	663	13	BU679690	BU679690 UI-C-EC1
c 33	660	17.6	660	13	BU733517	BU733517 UI-S-CQ1-
c 34	657.2	17.6	736	14	CB962566	CB962566 AGNCOURT
c 35	657	17.6	657	12	BM968524	BM968524 UI-CK-EC1
c 36	653.8	17.5	657	13	BU730180	BU730180 UI-S-CKI-
37	649.6	17.4	836	10	BF340950	BF340950 602038263
c 38	648.8	17.3	664	12	BM971589	BM971589 UI-CK-EC1
39	643	17.2	668	12	BM687906	BM687906 UI-S-CKI-
40	642.4	17.2	645	13	BQ549647	BQ549647 602495747
41	641.8	17.2	828	10	BG432926	BG432926 602495747
c 42	635.4	17.0	656	12	BM984811	BM984811 UI-C-EC1
43	631.6	16.9	758	10	BG719490	BG719490 60260046
44	627.4	16.8	945	10	BG033829	BG033829 602301209
45	626	16.7	778	10	BE895149	BE895149 601436077

Search completed: October 21, 2003, 21:04:19
Job time : 5911.62 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 3345.39 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-9
Perfect score: 1308
Sequence: 1 atgttgtgtctcccaaat.....ccagcatttcacccagatga 1308

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*
4: gb_em:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

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	35	218	16.7	700	6	AX210048	Sequence
	36	216.4	16.5	186901	2	AF267167	Homo sapi
	37	215	16.4	215	6	AX210028	Sequence
	38	214	16.4	2333	6	AX210036	Sequence
	39	205.4	15.7	700	6	AX210050	Sequence
	40	201.4	15.4	203	6	AX210030	Sequence
	41	191.4	14.6	65493	2	AC099807	Homo sapi
	42	178.2	13.6	1003	5	AF176665	Xenopus l
	43	174.6	13.3	194355	2	AC116511	Mus muscu
c	44	169.8	12.0	270745	2	AC097544	Rattus no
	45	161.4	12.3	4021	9	AB016317	Homo sapi

ALIGNMENTS

RESULT 1

LOCUS	AX210037		3742 bp	DNA	linear	PAT 31-AUG-2001
DEFINITION	Sequence	53 from Patent WO0157209.				
ACCESSION	AX210037					
VERSION	AX210037.1	GI:15424423				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	Nahmias,C., Stroberg,A.D. and Nouet,S.				
AUTHORS	Novel family of proteins, called atip, nucleic sequences coding for					
TITLE	same and uses thereof					
JOURNAL	Patent: WC 0157209-A 53 09-AUG-2001;					
	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)					
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Query Match	100.0%;	Score 1308;	DB 6;	Length 3742;
Best Local Similarity	100.0%;	Pred. No. 1.6e-286;		

Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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VERSION AF293357.1 GI:17224595
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SOURCE Homo sapiens (human)
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REFERENCE 1 (bases 1 to 1977)
AUTHORS Nouet, S. and Nahmias, C.
TITLE Cloning of human A22 receptor-interacting protein 1 (ATIP1)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1977)
AUTHORS Nouet, S. and Nahmias, C.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2000) Institut Cochin de Genetique Moleculaire,
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 AUTHORS Seibold,S., Rudloff,C., Weber,M., Galle,J., Warner,C. and Marx,M.
 TITLE Identification of a new tumor suppressor gene located at chromosome
 8p21.3-22
 JOURNAL FASEB J. (2003) In press
 PUBMED 12692079
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 AUTHORS Seibold,S. and Marx,M.
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 Osterheimer Str. 200, Cologne 51109, Germany
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 AUTHORS Seibold,S. and Marx,M.
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DEFINITION	Sequence 50 from Patent W00185942.		
ACCESSION	AX301208		
VERSION	AX301208.1	GI:17382299	
KEYWORDS			
SOURCE	homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Yue,H., Tang,Y.T., Au-Young,J., Lu,D.A., Baughn,M.R., Hillman,J.L., Azimzai,Y., Lal,P., Yao,M.G., Bandman,C., Burford,N., Batra,S., Kearney,L. and Policky,J.L.		
TITLE	Cytoskeleton-associated proteins		
JOURNAL	Patent: WO 018942-A 50 15-NOV-2001; Incyte Genomics, Inc. (US) Location/Qualifiers		
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Best Local Similarity	99.6%	Prod. No. 7.9e-293;		
Matches 1306;	Conservative 0;	Mismatches 2;	Indels 3;	Gaps 1;
QY	1	ATGTGTTCTCTCCCAATTTCTCTTAACCAACATTCACATACGACTGAACGCGCAAGA	60	
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QY	121	GTTCGAAAGAGGAGCAAAAGATCTCGAGCTTATGTATCCAGCCACAGACGTCCC	180	
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QY	301	GCATTACAGACTTGATTCACGACCTGCTGTCGAGCGGAGAGACACTGAAACACAC	360	
DB	584	GCATTACAGACTTGATTCACGACCTGCTGTCGAGCGGAGAGACACTGAAACACAC	643	
QY	361	AAACCCCTATCTCAGAACTGTGTTAACTCCGGGAGAGCTAGTCACTTGCTTCAACAC	420	
DB	644	AAACCCCTATCTCAGAACTGTGTTAACTCCGGGAGAGCTAGTCACTTGCTTCAACAC	703	
QY	421	TGTGACAAATTAGAAAGCCAGGATGAGTTACAAACAGTGTATGAGACATTCGTCAG	480	
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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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maxlen: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Job time : 3348.39 secs

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	100.0	1308	21	AAZ99092 Human ATIP coding
2	1308	100.0	3742	21	AAZ99091 Human ATIP gene.
3	1308	100.0	3742	22	AAH74362 Nucleotide sequence
4	1291.8	98.8	1615	24	AAZ99905 Polynucleotide enc
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7	1177.4	90.0	3807	25	ABX10230 Human cDNA encodi
8	1177.4	90.0	4937	25	ABX63076 Human cDNA #76 di
9	1176.2	89.9	3315	22	AAH19632 Human cDNA sequen
10	1175.8	89.9	1369	22	AAH74322 Nucleotide sequenc
11	1175.8	89.9	1458	22	AAH74325 Nucleotide sequenc
12	1174.2	89.8	5799	22	AAH74383 Nucleotide sequenc
13	1173.4	89.7	1191	22	AAH74326 Nucleotide sequenc
14	1172.6	89.6	5961	22	AAH74385 Nucleotide sequenc
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21	509.2	38.9	656	22	AAZ26578 Human cDNA encodin
22	509.2	38.9	656	25	ABX73919 Human novel polynu
23	457.6	35.0	791	25	AAZ53121 Human genomic DNA
24	449.6	34.4	481	22	AAZ26163 Human cDNA encodin
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26	234.6	17.9	242	25	ABX74609 Human cDNA sequenc
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ALIGNMENTS

RESULT 1	
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XX	AC AAZ99092;
XX	DT 21-JUN-2000 (first entry)
XX	DE Human ATIP coding sequence.
XX	KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
XX	KW two-hybrid screen; signal transduction; human.
XX	OS Homo sapiens.
XX	FN FR2782084-A1.
XX	PD 11-FEB-2000.
XX	PF 04-AUG-1998; 98FR-0009997.
XX	PR 04-AUG-1998; 98FR-0009997.
XX	(CNRS) CNRS CENT NAT RECH SCI.
XX	PI Elbaz N, Nahmias C, Strosberg AD;
XX	DR WPI; 2000-248410/22.
XX	PT Nucleic acids coding for angiotensin II receptor AT2 interacting
XX	PT proteins useful in screening assays for receptor-protein interaction -
XX	PS Claim 1; Page 40-41; 63pp; French.
XX	CC This sequence represents the open reading frame (ORF) from the cDNA
XX	CC encoding a human angiotensin II (AT2) receptor interactive protein
XX	CC (ATIP; AAY83780). The human gene was isolated using a fragment of the
XX	CC mouse gene (AAZ99088). Cells transformed with vectors containing the
XX	CC cDNA, or immobilized proteins encoded by it, can be used to screen for
XX	CC substances that modulate ATIP-AT2 interaction or substances that interact
XX	CC with ATIP, especially using yeast two- or three-hybrid techniques. Such
XX	CC substances may be useful for treating disorders associated with anomalous
XX	CC AT2 receptor signal transduction.
SQ	Sequence 1308 BP; 460 A; 277 C; 294 G; 277 T; 0 other;
Query Match 100.0%; Score 1308; DB 21; Length 1308;	
Best Local Similarity 100.0%; Pred. No. 1.3e-314;	
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 2

AAZ99091
ID AAZ99091 standard; cDNA; 3742 BP.
XX
AC AAZ99091;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human ATIP gene.
XX
KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
KW two-hybrid screen; signal transduction; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 293..1600
FT /*tag= a
FT /product= "human ATIP"
FT /note= "angiotensin II (AT2) receptor interactive
XX protein"
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XX (CNRS) CNRS CENT NAT RECH SCI.
PA

XX Elbaz N, Nahmias C, Strosberg AD;
PI WPI: 2000-248410/22.
DR P-PSDB; AAY63780.
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
PT proteins useful in screening assays for receptor-protein interaction -
XX Claim 1; Fig 4; 63pp; French.
XX This sequence represents the cDNA encoding a human angiotensin II (AT2)
CC receptor interactive protein (ATIP). The gene was isolated using a
CC fragment of the mouse gene (AA299088). Cells transformed with vectors
CC containing the cDNA, or immobilized proteins encoded by it, can be used
CC to screen for substances that modulate ATIP-AT2 interaction or
CC substances that interact with ATIP, especially using yeast two- or
CC three-hybrid techniques. Such substances may be useful for treating
CC disorders associated with anomalous AT2 receptor signal transduction.
XX Sequence 3742 BP; 1180 A; 762 C; 793 G; 1007 T; 0 other;
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Query Match 100.0%; Score 1308; DB 21; Length 3742;
Best Local Similarity 100.0%; Pred. No. 1.3e-314; Indels 0; Gaps 0;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
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ID AAS99905 standard; cDNA; 1615 BP.
XX
AC AAS99905;
XX
DT 12-MAR-2002 (first entry)
XX
DE Polynucleotide encoding human cytoskeleton-associated protein #16.
XX
KW Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder; ss;
KW cell proliferative disorder; inflammatory disorder; prion disease;
KW vesicle trafficking disorder; gastrointestinal disorder; muscle disorder;
KW neurological disorder; cell motility disorder; reproductive disorder;
KW spinal cord disease; central nervous system disorder; mental disorder;
KW gene therapy; cancer.
XX
OS Homo sapiens.
XX
FN W0200185942-A2.
XX
PD 15-NOV-2001.
XX
PP 03-MAY-2001; 2001WO-US14355.

XX 05-MAY-2000; 2000US-201960P.
PR 08-MAY-2000; 2000US-20729P.
PR 05-JUN-2000; 2000US-209705P.
PR 07-JUN-2000; 2000US-210149P.
XX 21-JUN-2000; 2000US-213215P.
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Tang YT, Au-Young J, Lu DAM, Baughn MS, Hillman JL;
PI Azimtai Y, Ial P, Yao MG, Bandman O, Burford N, Batra S;
PI Kearney L, Policky JL;
XX
DR WPI; 2002-062248/08.
DR P-PSDB; AAU74345.
XX
PI New cytoskeleton-associated proteins and polynucleotides, useful for
PI diagnosing, preventing and treating cell proliferative, autoimmune,
PI inflammatory, neurological, cell motility, reproductive and muscle
PI disorders -
XX
PS Claim 5; Page 180; 194pp; English.
XX
CC The invention relates to human cytoskeleton-associated polypeptides
CC (CYSKP) and their associated polynucleotide sequences. The sequences are
CC useful in the treatment of disorders associated with overexpression or
CC underexpression of CYSKP in a patient. The disorders include cell
CC proliferative disorders (such as cancer, actinic keratosis,
CC arteriosclerosis, cirrhosis, hepatitis and psoriasis),
CC autoimmune/inflammatory disorders (such as, asthma, atherosclerosis,
CC osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus
CC and anaemia), vesicle trafficking disorders (such as
CC hypercholesterolaemia, diabetes insipidus, Gravel's disease and goitre),
CC gastrointestinal disorders, prion diseases, neurological disorders (such
CC as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC and other motor neuron disorders), cell motility disorders, reproductive
CC disorders (such as endometriosis and polycystic ovary syndrome), muscle
CC disorders (such as myocarditis, migraine, hypertension, hypoglycaemia,
CC myocardial infarction, epilepsy and muscular dystrophy), spinal cord
CC diseases, central nervous system disorders (such as Down syndrome and
CC cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
CC Sequences AAS99890-AAS99923 represent cDNA molecules encoding human
XX CYSKP of the invention.
SQ Sequence 1615 BP; 540 A; 344 C; 370 G; 361 T; 0 other;
Query Match 96.8%; Score 1291.8; DB 24; Length 1615;
Best Local Similarity 99.6%; Pred. No. 1.2e-310;
Matches 1306; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 1 ATGTTGTTGCTCCCAATTCCTTATCCACCATTCACATAGACTGAGCGCAAGG 60
|||||
Db 284 ATGTTGTTGCTCCCAATTCCTTATCCACCATTCACATAGACTGAGCGCAAGG 343
|||||
QY 61 TTCTTGGAAACCTTCGACTTCCTTCAGGGTTTAGGAGAACCTGTGTTTCCAGCA 120
|||||

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 2062.19 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-9
Perfect score: 1308
Sequence: 1 atgttggttcccaatt.....ccagcattccaccagatga 1308

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562794

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_estl:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943.4	72.1	2477	11 AK030510	AK030510 Mus muscu
2	927.4	70.9	3963	11 AK031693	AK031693 Mus muscu
3	819.4	62.6	1005	13 B0070423	B0070423 AGENCOURT
4	740	56.6	830	9 AUI38373	AUI38373 AUI38373
5	728.2	55.7	1346	11 B0007328	B0007328 Homo sapi
6	692.6	53.0	3237	11 AK035576	AK035576 Mus muscu
7	675.2	51.6	782	9 AUI141757	AUI141757 AUI141757
8	631.6	48.3	758	10 B0719490	B0719490 602690048
9	626	47.9	778	10 B0895149	B0895149 601436077
10	622.6	47.6	950	13 B0921402	B0921402 AGENCOURT
11	618.4	47.3	945	10 B0033829	B0033829 602201209
12	608.4	46.5	626	12 B0737916	B0737916 K-EST0001
13	600.4	45.9	650	12 B0983699	B0983699 UI-CF-DUI
14	580	44.3	600	12 B0311947	B0311947 ig64c02.y
15	541.4	41.4	645	13 B0549647	B0549647 ik99f06.x
16	539.4	41.2	557	10 B0552421	B0552421 hw26b02.x
17	504	38.5	889	10 B0574166	B0574166 602131321
18	484.8	37.1	990	13 B0893803	B0893803 AGENCOURT
19	479.4	36.7	495	9 AA702088	AA702088 zif90f09.s
20	479.4	36.7	495	9 AA723012	AA723012 zh30e09.s
21	473.8	36.2	845	9 AUI31191	AUI31191 AUI31191
22	471.4	36.0	510	9 AUI94721	AUI94721 rz32b12.s
23	467.2	35.7	486	9 AA778812	AA778812 zj38a04.s
24	467	35.7	582	10 B0573578	B0573578 602595386
25	455.6	34.8	490	12 B0011508	B0011508 UI-1-BC1P
26	451.2	34.5	920	13 B0523654	B0523654 AGENCOURT
27	443.4	33.9	461	9 A1564089	A1564089 tn57b04.x
28	430.6	32.9	748	10 B0141309	B0141309 601789830
29	424.2	32.4	836	10 B0340950	B0340950 602038263
30	420.8	32.2	734	14 CB316595	CB316595 AGENCOURT
31	416.8	31.9	541	4 B0512030	B0512030 RZPD MUs
32	414	31.7	430	9 A1149364	A1149364 gc82c04.x
33	410.6	31.4	454	10 A0994317	A0994317 PM3-HN001
34	410.6	31.4	776	13 B0387252	B0387252 603856971
35	410	31.3	426	9 A1626069	A1626069 ar87f04.x
36	407.6	31.2	600	13 B0921755	B0921755 6093-85 M
37	396.4	30.3	422	10 B0515637	B0515637 UI-H-BW1-
38	395	30.2	440	14 CB128270	CB128270 K-EST0177
39	388.4	29.7	624	12 B0951991	B0951991 UI-M-EH0-
40	387	29.6	507	9 A1363967	A1363967 qk34e06.x
41	386.4	29.5	657	10 B0628131	B0628131 BB628131
42	385.8	29.5	405	9 A1879905	A1879905 ar99c-9.x
43	384.8	29.4	862	13 B0248050	B0248050 6037-1419
44	379.6	29.0	782	13 B0702398	B0702398 UI-M-F10-
45	378.4	28.9	820	13 B0344537	B0344537 6035-2603

CM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 84.402 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcgatccacagacagacgggaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 204581386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
1	24	72.7	1323	10	AY246699	Mus muscu
2	24	72.7	1803	10	AF173360	Mus muscu
3	24	72.7	3629	10	BC043321	Mus muscu
4	24	72.7	5218	10	BC041777	Mus muscu
5	24	72.7	5219	10	BC042206	Mus muscu
6	24	72.7	194355	2	AC116511	Mus muscu
7	21.4	64.8	1920	6	AX139914	Sequence
8	21.4	64.8	1920	6	BD013824	Promoter
9	21.4	64.8	5800	1	ILZ97015	Lactococcus
10	21.4	64.8	9840	6	AX139909	Sequence
11	21.4	64.8	9840	6	BD013820	Promoter
12	21.4	64.8	205187	2	AC137156	Mus muscu
13	21.4	64.8	223132	10	AC123870	Mus muscu
14	21.4	64.8	251396	2	AC128362	Mus muscu
15	21.4	64.8	254304	2	AC133760	Rattus no
16	21.2	64.2	307349	2	AC115785	Mus muscu
17	21	63.6	242130	2	AC108556	Rattus no
18	20.8	63.0	1323	10	AY208915	Rattus no
19	20.8	63.0	130665	10	AF289666	Mus muscu
20	20.8	63.0	166045	2	AC134957	Tetraodon
21	20.8	63.0	201605	10	AF289667	Mus muscu
22	20.8	63.0	203602	10	AF325177	Mus muscu
23	20.8	63.0	263706	2	AC097149	Rattus no
24	20.8	63.0	270745	2	AC097544	Rattus no
25	20.6	62.4	2879	1	AB027515	Erythroba
26	20.6	62.4	70751	2	AC101724	Mus muscu
27	20.6	62.4	232976	2	AC116557	Mus muscu
28	20.6	62.4	301276	1	AE016758	Escherich
29	20.4	61.8	1496	5	AY219410	Salvelinu
30	20.4	61.8	9698	1	AE012025	Xanthomon
31	20.4	61.8	127376	2	AC141672	Apis mell
32	20.4	61.8	220998	2	AC102965	Rattus no
33	20.4	61.8	226193	2	AC120679	Rattus no

c 34 20.4 61.8 242366 2 AC121386 Rattus no
c 35 20.4 61.8 244696 2 AC103554 Rattus no
c 36 20.2 3068 6 E09269 Male-specif
c 37 20.2 3068 6 E12118 E12118 Repeated se
c 38 20.2 3068 6 I15249 I15249 Sequence 3
c 39 20.2 3068 6 I62883 I62883 Sequence 3
c 40 20.2 61.2 66658 2 AC110649_3 Continuation 1 of
c 41 20.2 61.2 110000 2 AC110649_2 Continuation 1 of
c 42 20.2 229635 2 AC094256 Rattus no
c 43 20.2 61.2 253729 2 AC094816 Rattus no
c 44 20.2 61.2 256344 2 AC127789 Rattus no
c 45 20.2 61.2 269267 2 AC110861 Rattus no

Search completed: October 21, 2003, 17:18:12
Job time : 88.402 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:56:18 ; Search time 6.34512 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcgataccagacagacgcgacggaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	33	100.0	33	21	Mouse ATIP gene pr
2	24	72.7	354	21	Mouse ATIP coding
3	24	72.7	1323	21	Mouse ATIP coding
4	24	72.7	1803	21	Mouse ATIP gene.
5	21.4	64.8	9840	22	Murine neuroleptid
6	20.2	61.2	3068	14	Sequence which hyb
7	20.2	61.2	3068	17	Bovine Y chromosom
8	20	60.6	852	23	DNA encoding novel
9	20	60.6	879	21	Arabidopsis thalia
10	20	60.6	1035	21	Arabidopsis thalia
11	19.4	58.8	275	24	Mouse ES cell rela
12	19	57.6	2255	23	Arabidopsis thalia
13	19	57.6	47066	23	Drosophila melanog
14	18.8	57.0	694	22	Novel human polyu
15	18.8	57.0	659158	25	Mouse high g-cath
16	18.6	56.4	560	22	Human cDNA clone (
17	18.6	56.4	2219	22	Human cDNA sequenc
18	18.6	56.4	169998	24	Human Her-1 gene.
19	18.6	56.4	197496	24	Human EGFR SEJ ID
20	18.4	55.8	1398	23	Drosophila melanog
21	18.4	55.8	3629	23	Drosophila melanog
22	18.4	55.8	8605	22	Human polyucl.eoti
23	18.4	55.8	9408	19	Human BAZ2-alpha c
24	18.2	55.2	240	25	Group III cDNA can
25	18.2	55.2	283	25	Group III cDNA can
26	18.2	55.2	392	21	Human secreted pro
27	18.2	55.2	563	24	FLJ200100flis clone
28	18.2	55.2	625	25	Human GENSET codin
29	18.2	55.2	640	25	Human GENSET codin
30	18.2	55.2	867	24	Arabidopsis thalia
31	18.2	55.2	1200	21	Arabidopsis thalia
32	18.2	55.2	1424	22	Human ORFX ORF3051
33	18.2	55.2	1447	21	Drosophila melanog
34	18.2	55.2	2680	23	Drosophila melanog
35	18.2	55.2	3150	23	Human immune/haema
36	18.2	55.2	4502	22	Drosophila melanog
37	18.2	55.2	6130	23	Human immune/haema
38	18.2	55.2	9475	22	Human immune/haema
39	18.2	55.2	201143	24	Human DNA differen
40	18	54.5	4013	22	Corynebacterium th
41	18	54.5	39328	24	Human lipase endot
42	18	54.5	4403765	22	Mycobacterium tube
43	18	54.5	4411529	22	Mycobacterium tube
44	17.8	53.9	362	21	Human secreted pro
45	17.8	53.9	381	21	Human secreted pro

ALIGNMENTS

RESULT 1
AAZ99094

AAZ99094;

DE Mouse ATIP gene primer oligo.sens.

Mus sp.

PD 11-FEB-2000.

PR 04-AUG-1998; 98FR-0009997.

Elbaz N, Nahmias C, Strosberg AD;

PT Nucleic acids coding

Primers AAZ99094-Z99095 were used

Sequence 33 BP; 9 A; 10 C; 12 G; 2 T; 0 other:

Best local similarity 100.00; freq. NO: 0.00022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
1 CGGGATCCAGACAGACCGGACCGAACTGGAG 33

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 6.75201 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-11

Perfect score: 33
Sequence: 1 cggatccagacagacggagcgaactggag 33

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
--------	-------	-------	-------	--------	----	-------------

1	19.4	58.8	275	9	US-09-728-446-581	Sequence 581, App
2	19.2	58.2	263	13	US-10-027-632-143193	Sequence 143193, App
c 3	19.2	58.2	581	13	US-10-027-632-134093	Sequence 134093, App
c 4	19.2	58.2	581	13	US-10-027-632-134094	Sequence 134094, App
5	19.2	58.2	640	13	US-10-027-632-143192	Sequence 143192, App
6	19.2	58.2	820	13	US-10-027-632-143189	Sequence 143189, App
7	19.2	58.2	820	13	US-10-027-632-143191	Sequence 143191, App
c 8	19.2	58.2	854	13	US-10-027-632-173748	Sequence 173748, App
c 9	19.2	58.2	897	14	US-10-156-761-357	Sequence 357, App
c 10	19.2	58.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 11	18.8	57.0	587	12	US-10-029-386-4316	Sequence 4316, Ap
c 12	18.8	57.0	659158	10	US-09-771-208-20	Sequence 20, Appl
c 13	18.6	56.4	197496	10	US-09-877-177-10	Sequence 10, Appl
c 14	18.4	55.8	573	14	US-10-156-761-7365	Sequence 7365, Ap
c 15	18.4	55.8	3071	13	US-10-027-632-114585	Sequence 114585, A
c 16	18.4	55.8	715517	13	US-10-027-632-53712	Sequence 53712, A
17	18.2	55.2	474	11	US-09-918-995-21180	Sequence 21180, A
c 18	18.2	55.2	480	11	US-09-918-995-13907	Sequence 13907, A
c 19	18.2	55.2	867	9	US-09-770-445-571	Sequence 571, App
c 20	18.2	55.2	888	14	US-10-156-761-2936	Sequence 2936, Ap
c 21	18.2	55.2	1416	14	US-10-156-761-4207	Sequence 4207, Ap
c 22	18.2	55.2	2322	12	US-09-814-353-19200	Sequence 19200, A
c 23	18.2	55.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 24	18	54.5	514	13	US-10-027-632-46468	Sequence 46468, A
c 25	18	54.5	599	13	US-10-027-632-67722	Sequence 67722, A
c 26	18	54.5	599	13	US-10-027-632-67747	Sequence 67747, A
c 27	18	54.5	599	13	US-10-027-632-295388	Sequence 295388, A
c 28	17.8	53.9	428	11	US-09-918-995-1571	Sequence 1571, Ap
c 29	17.8	53.9	860	13	US-10-027-632-120951	Sequence 120951, A
c 30	17.8	53.9	860	13	US-10-027-632-120952	Sequence 120952, A
c 31	17.8	53.9	860	13	US-10-027-632-120953	Sequence 120953, A
c 32	17.8	53.9	1800	14	US-10-156-761-856	Sequence 856, App
c 33	17.8	53.9	1875	14	US-10-156-761-7458	Sequence 7458, Ap
c 34	17.8	53.9	2085	14	US-10-156-761-6252	Sequence 6252, Ap
c 35	17.8	53.9	2358	14	US-10-043-487-59	Sequence 59, Appl
c 36	17.8	53.9	2797	14	US-10-060-036-46	Sequence 46, Appl
37	17.8	53.9	11962	10	US-09-905-129-20	Sequence 20, Appl
38	17.8	53.9	11962	10	US-09-991-630-20	Sequence 20, Appl
39	17.8	53.9	11967	10	US-09-905-129-3	Sequence 3, Appli
40	17.8	53.9	11967	10	US-09-991-630-3	Sequence 3, Appli
c 41	17.8	53.9	14646	12	US-09-873-319-691	Sequence 691, App
c 42	17.8	53.9	14646	12	US-09-960-706-1043	Sequence 1043, Ap
43	17.6	53.3	157	12	US-10-029-386-18917	Sequence 18917, A
c 44	17.6	53.3	292	11	US-09-968-433-56	Sequence 56, Appl
45	17.6	53.3	535	12	US-10-029-386-5161	Sequence 5161, Ap

Search completed: October 22, 2003, 04:13:27
Job time : 2323.75 secs

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 52.0277 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-11
Perfect score: 33
Sequence: 1 cgcggatccacagacagcggagcgaactggag 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:**
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:**

28: gb_gss1:**
29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	352	13	BY068750
2	24	72.7	358	9	AI466472
3	24	72.7	364	13	BY130313
4	24	72.7	380	10	BE449013
5	24	72.7	487	10	BF535672
6	24	72.7	500	9	AA880300
7	24	72.7	517	10	BE632532
8	24	72.7	560	14	CD565243
9	24	72.7	624	12	BM951991
10	24	72.7	657	10	BB628131
11	24	72.7	670	10	BB636465
12	24	72.7	710	14	CE723104
13	24	72.7	782	13	BU702398
14	24	72.7	950	13	BQ921402
15	24	72.7	2477	11	AK030510
16	24	72.7	3237	11	AK035576
17	24	72.7	3963	11	AK031693
18	23	69.7	530	13	BQ830956
19	22.4	67.9	732	14	CE246442
20	22.2	67.3	1201	13	EX334102
21	21.4	64.8	688	28	BH969640
22	21.4	64.8	701	10	BF468054
23	21.4	64.8	954	14	CE203504
24	21.2	64.2	908	10	BG107884
25	21	63.6	368	12	BI975959
26	21	63.6	1083	29	CNS055M0
27	20.8	63.0	376	14	CE691075
28	20.8	63.0	560	12	BJ217670
29	20.8	63.0	809	10	BF973404
30	20.8	63.0	875	10	BE410275
31	20.6	62.4	417	13	BY458150
32	20.6	62.4	462	10	BF951635
33	20.6	62.4	896	14	CD360742
34	20.4	61.8	131	26	BH712463
35	20.4	61.8	299	28	BH604194
36	20.4	61.8	348	28	BH459603
37	20.4	61.8	360	28	BH496990
38	20.4	61.8	380	28	BH494004
39	20.4	61.8	399	28	BH743660
40	20.4	61.8	430	9	AI222038
41	20.4	61.8	509	28	BH682274
42	20.4	61.8	512	28	BH682764
43	20.4	61.8	536	28	BH497338
44	20.4	61.8	550	28	BH556094
45	20.4	61.8	557	28	BH508195

OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 08:57:52 ; Search time 86.9596 Seconds
(without alignments)
15995.091 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cgggaattcaactacaacatttggttaaacgac 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	22.2	65.3	1323	10 AY208915	AY208915 Rattus no
c 2	22.2	65.3	1323	10 AY246699	AY246699 Mus muscu
c 3	22.2	65.3	1803	10 AF173380	AF173380 Mus muscu
c 4	22.2	65.3	3629	10 BC043321	BC043321 Mus muscu
c 5	22.2	65.3	5218	10 BC041777	BC041777 Mus muscu
c 6	22.2	65.3	5219	10 BC042206	BC042206 Mus muscu
c 7	22.2	65.3	194355	2 AC116511	AC116511 Mus muscu
c 8	22.2	65.3	270745	2 AC097544	AC097544 Rattus no
c 9	21.8	64.1	180366	9 AC036196	AC036196 Homo sapi
c 10	21.8	64.1	183015	2 AC140064	AC140064 Homo sapi
c 11	21.8	64.1	194996	9 AC103858	AC103858 Homo sapi
c 12	21.8	64.1	222710	2 BX470169	BX470169 Danio rer
c 13	21.6	63.5	246099	2 AC106365	AC106365 Rattus no
c 14	21.4	62.9	43469	3 CER0757	275955 Caenorhabdi
c 15	21.4	62.9	111103	9 AC007129	AC007129 Homo sapi
c 16	21.4	62.9	122351	9 AC023157	AC023157 Homo sapi
c 17	21.4	62.9	130377	2 AC122130	AC122130 Homo sapi
c 18	21.4	62.9	148481	2 AC122139	AC122139 Homo sapi
c 19	21.4	62.9	189209	2 AC099649	AC099649 Homo sapi
c 20	21.4	62.9	192343	2 AC126596	AC126596 Mus muscu
c 21	21.4	62.9	195743	2 AC016774	AC016774 Homo sapi
c 22	21.4	62.9	203842	9 AC010789	AC010789 Homo sapi
c 23	21.4	62.9	228736	2 AC136565	AC136565 Rattus no
c 24	21.4	62.9	262820	2 AC137354	AC137354 Rattus no
c 25	21.4	62.9	263406	2 AC129276	AC129276 Rattus no
c 26	21.4	62.9	267668	2 AC133021	AC133021 Rattus no
c 27	21.4	62.9	271639	2 AC137481	AC137481 Rattus no
c 28	21.2	62.4	272	11 G70578	G70578 VEO024311FB
c 29	21.2	62.4	291	11 G71357	G71357 VEO024311FM
c 30	21.2	62.4	300	11 G71180	G71180 VEO182311FM
c 31	21.2	62.4	328	11 G70613	G70613 VEO182311FB
c 32	21.2	62.4	172358	2 AC120612	AC120612 Rattus no
c 33	21	61.8	172193	2 AC113567	AC113567 Canis fam

c 34	21	61.8	177015	9 AC108137	AC108137 Homo sapi
c 35	21	61.8	224735	2 AC132661	AC132661 Rattus no
c 36	21	61.8	227633	2 AC095513	AC095513 Rattus no
c 37	21	61.8	233886	2 AC128261	AC128261 Rattus no
c 38	21	61.8	244042	2 AC103004	AC103004 Rattus no
c 39	21	61.8	290791	2 AC137023	AC137023 Rattus no
c 40	21	61.8	305488	2 AC111881	AC111881 Rattus no
c 41	20.8	61.2	659	11 G73168	G73168 DA2-SNV_IV
c 42	20.8	61.2	4773	14 PPV6GP	X56258 Plum Fox Vi
c 43	20.8	61.2	40133	9 AC073331	AC073331 Homo sapi
c 44	20.8	61.2	40328	9 H5AC000021	AC000021 Origins o
c 45	20.8	61.2	43795	9 AC000022	AC000022 Genom's s

Search completed: October 21, 2003, 17:18:16
Job time : 90.9596 secs

OM nucleic - nucleic search, using sw model
Run on: October 21, 2003, 08:56:18 ; Search time 6.5374 Seconds
(without alignments)
14039.364 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cggaaattactacaaccttcgtttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	100.0	34	21	Mouse A1IP gene pr
c 2	22.2	65.3	1323	21	Mouse A1IP coding
c 3	22.2	65.3	1803	21	Mouse A1IP gene.
c 4	21.4	62.9	32169	22	Human nervous syst
c 5	21.4	62.9	32169	22	Human testicular a
c 6	21.4	62.9	32169	23	Human nervous syst
c 7	21.4	62.9	32189	22	Human reproductive
c 8	21.4	62.9	32189	22	Human testicular a
c 9	21.4	62.9	32189	23	Human immune/haema
c 10	21.4	62.9	33971	22	Corn tassal-deriva
c 11	21.2	62.4	287	24	Mouse A1IP coding
c 12	21	61.8	354	21	Human DAZ genomic
c 13	20.8	61.2	40328	21	Human DAZ genomic
c 14	20.8	61.2	43795	21	Human DAZ genomic
c 15	20.4	60.0	1463	24	Pasteurella haemol
c 16	20.2	59.4	262	21	Rat hepatocyte car
c 17	20.2	59.4	1026	20	Human secreted pro
c 18	19.8	58.2	252	25	Human GDP-mannose
c 19	19.8	58.2	288	25	Human GDP-mannose
c 20	19.8	58.2	387	22	Human polynucleoti
c 21	19.8	58.2	2176	22	Human cDNA sequenc
c 22	19.6	57.6	583	24	Arabidopsis thalia
c 23	19.6	57.6	820	25	Human colon specif
c 24	19.6	57.6	839	25	Human colon specif
c 25	19.6	57.6	8078	22	Tumour suppressor
c 26	19.4	57.1	348	23	Human prostate exp
c 27	19.4	57.1	349	23	Human prostate exp
c 28	19.4	57.1	400	23	Human prostate exp
c 29	19.4	57.1	400	23	Human prostate exp
c 30	19.4	57.1	418	23	Human prostate exp
c 31	19.4	57.1	465	23	Human prostate exp
c 32	19.4	57.1	465	23	Human prostate exp
c 33	19.4	57.1	465	23	Human prostate exp
c 34	19.4	57.1	607	24	Oligonucleotide fo
c 35	19.4	57.1	607	24	Oligonucleotide fo
c 36	19.4	57.1	800	23	Human prostate exp
c 37	19.4	57.1	801	23	Human prostate exp
c 38	19.4	57.1	801	23	Human prostate exp
c 39	19.4	57.1	801	23	Human prostate exp
c 40	19.4	57.1	801	23	Human prostate exp
c 41	19.4	57.1	801	23	Human prostate exp
c 42	19.4	57.1	1519	22	Arabidopsis thalia
c 43	19.4	57.1	2948	23	Arabidopsis thalia
c 44	19.4	57.1	8934	23	Drosophila melanog
c 45	19.2	56.5	452	21	N. meningitidis pa

ALIGNMENTS

RESULT 1
 AAZ99095
 ID AAZ99095 standard; DNA; 34 BP.
 XX
 AC AAZ99095;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Mouse ATIP gene primer oligo.antisens.
 XX
 KW Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ss;
 KW two-hybrid screen; signal transduction; PCR primer.
 XX
 OS Mus sp.
 XX
 FN FR2762084-A1.
 XX
 PD 11-FEB-2000.
 XX
 PF 04-AUG-1998; 98FR-0009997.
 XX
 PR 04-AUG-1998; 98FR-0009997.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Elbaz N, Nahmias C, Strosberg AD;
 XX
 DR WPI; 2000-248410/22.
 XX
 PT Nucleic acids coding for angiotensin II receptor AT2 interacting
 PT proteins useful in screening assays for receptor-protein interaction -
 XX
 PS Claim 4; Page 16; 63pp; French.
 XX
 CC Primers AAZ99094-299095 were used to PCR amplify the cDNA encoding a
 CC mouse angiotensin II (AT2) receptor interactive protein (ATIP; AA83777).
 CC The initial clone (AAZ99090) was isolated from a two-hybrid screen using
 CC the C-terminal fragment of the mouse AT2 receptor as the "bait"
 CC (AA83781). The "target" is a mouse foetal cDNA library. Cells
 CC transformed with vectors containing the cDNA, or immobilized proteins
 CC encoded by it, can be used to screen for substances that modulate
 CC ATIP-AT2 interaction or substances that interact with ATIP, especially
 CC using yeast two- or three-hybrid techniques. Such substances may be
 CC useful for treating disorders associated with anomalous AT2 receptor
 CC signal transduction.
 XX
 SQ Sequence 34 BP; 10 A; 10 C; 4 G; 10 T; 0 other;
 Query Match 100.0%; Score 34; DB 21; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGAATTCACACACCTTCGTTTAAGCATC 34
 Db 1 CGGGAATTCACACACCTTCGTTTAAGCATC 34

c	1	21.4	62.9	32169	11	US-09-764-891-8605	Sequence 8605, Ap
c	2	21.4	62.9	32189	11	US-09-764-891-8604	Sequence 8604, Ap
c	3	21.2	62.4	254	9	US-09-923-876-1426	Sequence 1426, Ap
c	4	21.2	62.4	287	9	US-09-294-093B-4203	Sequence 4203, Ap
c	5	21	61.8	325	11	US-09-535-459-1205	Sequence 1205, Ap
c	6	20.2	59.4	1026	11	US-09-974-879-36	Sequence 36, Appl
c	7	20.2	59.4	1026	11	US-09-305-736-36	Sequence 36, Appl
c	8	19.8	58.2	252	10	US-09-878-574-10612	Sequence 10612, A
c	9	19.8	58.2	288	10	US-09-878-574-8275	Sequence 8275, Ap
c	10	19.8	58.2	875	13	US-10-632-121215	Sequence 121215, A
c	11	19.8	58.2	1572	11	US-09-918-624B-31	Sequence 31, Appl
c	12	19.6	57.6	583	10	US-09-938-842A-5265	Sequence 5265, Ap
c	13	19.6	57.6	729	13	US-10-027-632-111429	Sequence 111429, A
c	14	19.6	57.6	820	13	US-10-016-634A-26	Sequence 26, Appl
c	15	19.6	57.6	839	13	US-10-016-634A-27	Sequence 27, Appl
c	16	19.4	57.1	292	12	US-10-006-285-147	Sequence 147, App
c	17	19.4	57.1	504	12	US-10-006-285-339	Sequence 339, App
c	18	19.2	56.5	19972	12	US-10-311-455-79	Sequence 79, Appl
c	19	19.2	56.5	62804	13	US-10-096-960-3	Sequence 3, Appli
c	20	19	55.9	554	9	US-09-864-761-12250	Sequence 12250, A
c	21	19	55.9	624	13	US-10-027-632-248142	Sequence 248142, A
c	22	19	55.9	630	12	US-10-032-585-6392	Sequence 6392, Ap
c	23	19	55.9	77992	12	US-10-225-810-11	Sequence 11, Appl
c	24	19	55.9	250000	12	US-10-225-810-26	Sequence 26, Appl
c	25	19	55.9	322101	12	US-10-060-902-1	Sequence 1, Appli
c	26	18.8	55.3	438	13	US-10-027-632-74900	Sequence 74900, A
c	27	18.8	55.3	438	13	US-10-027-632-299653	Sequence 299653, A
c	28	18.8	55.3	736	13	US-10-027-632-144102	Sequence 144102, A
c	29	18.8	55.3	3655	13	US-10-027-632-259680	Sequence 259680, A
c	30	18.8	55.3	715517	13	US-10-027-632-53712	Sequence 53712, A
c	31	18.6	54.7	444	10	US-09-938-842A-412	Sequence 412, App
c	32	18.6	54.7	593	13	US-10-027-632-96754	Sequence 96754, A
c	33	18.6	54.7	593	13	US-10-027-632-306323	Sequence 306323, A
c	34	18.6	54.7	669	9	US-09-770-149-424	Sequence 424, App
c	35	18.6	54.7	1630	14	US-10-084-817-201	Sequence 201, App
c	36	18.6	54.7	2940917	13	US-10-027-632-174763	Sequence 174763, A
c	37	18.4	54.1	506	13	US-10-027-632-79342	Sequence 79342, A
c	38	18.4	54.1	506	13	US-10-027-632-301157	Sequence 301157, A
c	39	18.4	54.1	636	13	US-10-027-632-214275	Sequence 214275, A
c	40	18.4	54.1	710	13	US-10-027-632-151884	Sequence 151884, A
c	41	18.4	54.1	1126	13	US-10-027-632-249133	Sequence 249133, A
c	42	18.4	54.1	1126	13	US-10-027-632-249134	Sequence 249134, A
c	43	18.4	54.1	2470	13	US-10-027-632-260176	Sequence 260176, A
c	44	18.4	54.1	2747	9	US-09-778-927A-24	Sequence 24, Appl
c	45	18.4	54.1	1830121	14	US-10-329-960-1	Sequence 1, Appli

Search completed: October 22, 2003, 04:13:49
Job time : 28.9566 secs

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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 17:18:24 ; Search time 6.95661 Seconds
(without alignments)
13107.130 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 cgggaattactacaacattcgtttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues
Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 09:08:27 ; Search time 53.6043 Seconds
(without alignments)
15415.787 Million cell updates/sec

Title: US-09-762-194-12
Perfect score: 34
Sequence: 1 ccggaattactacaacotttggttaagcgc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estha:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_estl:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	22.8	67.1	276	9	AV296549
2	22.8	67.1	516	12	BW261570 daid6211
3	22.4	65.9	508	12	B3056698
4	22.4	65.9	628	10	B3056698
5	22.4	65.9	642	9	B3022525
c 6	22.2	65.3	450	14	B3022525 da095a09
c 7	22.2	65.3	509	12	AW767695 da77f06.x
c 8	22.2	65.3	517	10	CA556858 K0218E03
c 9	22.2	65.3	541	4	B1319660 iel4a05.y
c 10	22.2	65.3	600	13	B3652532 UI-M-AM0-
c 11	22.2	65.3	657	10	Bx512030 RZPD Mus
c 12	22.2	65.3	667	14	B0921755 6093-85 M
c 13	22.2	65.3	734	14	BB628131 BB628131
c 14	22.2	65.3	748	10	BY742653 BY742653
c 15	22.2	65.3	920	13	CB316595 AGENCOURT
c 16	22.2	65.3	950	13	BF141309 601789830
c 17	22.2	65.3	1090	29	B0523654 AGENCOURT
c 18	22.2	65.3	2477	11	BQ921402 AGENCOURT
c 19	22.2	65.3	3237	11	CC220629 CH261-1BA
c 20	22.2	65.3	3963	11	AK030510 Mus muscu
c 21	21.8	64.1	271	9	AK031693 Mus muscu
22	21.8	64.1	600	14	AX031693 Mus muscu
23	21.6	63.5	812	28	AI920645 614026801
c 24	21.4	62.9	1125	12	CA659570 wml.pK00
25	21.2	62.4	325	10	BH397605 AG-ND-133
26	21.2	62.4	263	9	BK464322 AGENCOURT
27	21.2	62.4	358	9	AI947351 614052G10
28	21.2	62.4	369	9	BG349168 947028F09
c 29	21.2	62.4	385	9	AW120381 614060A08
c 30	21.2	62.4	418	9	AW017677 614061G01
31	21.2	62.4	454	9	AW056048 660002A05
c 32	21.2	62.4	527	28	AW065792 614061G01
33	21.2	62.4	544	13	AI629809 486039D07
34	21.2	62.4	545	13	BH107504 RPCI-24-3
35	21.2	62.4	549	9	BQ668252 946134D05
c 36	21.2	62.4	554	9	BQ703374 946134H11
37	21.2	62.4	564	12	AI737756 605040H03
38	21.2	62.4	571	14	AW067499 660013C08
39	21.2	62.4	573	10	BK378462 MES1564-D
40	21.2	62.4	580	9	CD527810 3529.1.12
c 41	21.2	62.4	582	9	BE344835 946029D01
42	21.2	62.4	590	14	AW126505 614101E06
43	21.2	62.4	591	9	AW042241 614024501
44	21.2	62.4	592	28	CA398895 EL0140311
45	21.2	62.4	604	9	AI622281 486034D07
					AQ423423 CITR1-EI-
					AI491677 48602JF02

Search completed: October 21, 2003, 21:04:27
Job time : 56.6043 secs